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GenCore version 5.1.7

OM protein - protein search, using SW model

Run on: February 9, 2006, 03:18:06 ; Search time 270.325 Seconds
 (without alignments)
 425.847 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1995

Sequence: 1 MAQVQLQQSGAQLVRPGTSV.....GSEOKLISEBDLNHHHHH 262

Scoring table: BLOSUM62

Gapext 0.5

Searched: 2433163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:
 1: GeneseqP1980s: *
 2: GeneseqP1990s: *
 3: GeneseqP2000s: *
 4: GeneseqP2010s: *
 5: GeneseqP2012s: *
 6: GeneseqP2003as: *
 7: GeneseqP2003bs: *
 8: GeneseqP2004s: *
 9: GeneseqP2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1395	100.0	262	AAB70762	Single ch Ab70762 Single ch
2	1122	80.4	264	ABE29202	Multivale Human CD3
3	1002	71.8	248	AAW58826	Ab58826 Human CD3
4	946.5	67.8	562	ABR57058	Ab57058 Plasmid P
5	942.5	67.6	594	AEB19087	Ab19087 Immunokin
6	938	67.2	288	AAW82482	Abw82482 Mouse bis
7	936	67.1	288	AAW82317	Abw82317 Mouse bis
8	936	67.1	288	AAW82316	Abw82316 Mouse OKT
9	930	66.7	539	AAY50823	Aay50823 Fv-antibio
10	930	66.7	554	AAY50822	Aay50822 Fv-antibio
11	919.5	65.9	269	ADR10544	Adr10544 NPB polyp
12	917.5	65.8	283	ADP84526	Adp84526 V12scfv
13	911.5	65.3	267	ADR70320	Adr70320 Polioviru
14	909.5	65.2	267	ADP8454	Adp8454 Single ch
15	906	64.9	264	ADP84957	Adp84957 Single ch
16	905.5	64.9	263	ADP84958	Adp84958 Single ch
17	905.5	64.9	562	ABRS7059	Ab57059 Plasmid P
18	905	64.9	266	ADP84955	Adp84955 Single ch
19	904	64.8	262	ADP84959	Adp84959 Single ch
20	904	64.8	268	ADR70319	Adr70319 Polioviru
21	902.5	64.7	261	ADP84960	Adp84960 Single ch
22	902.5	64.7	265	ADP84956	Adp84956 Single ch
23	902	64.7	260	ADP84961	Adp84961 Single ch
24	901.5	64.6	259	ADP84962	Adp84962 Single ch

ALIGNMENTS

RESULT 1
 ID AAB70762 standard; protein; 262 AA.
 XX
 AC AAB70762;
 XX DT 18-MAY-2001 (first entry)

Single chain Fv antibody construct anti-CD16 VH domain protein.
 DB
 XX Single chain Fv antibody; anti-CD16; anti-CD30; VH domain;
 KW Single chain Fv antibody; anti-CD16 receptor; CD30 surface protein; cytostatic;
 KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
 KW tumor cell; natural killer cell activation; Hodgkin's disease;
 KW Reed-Sternberg disease.
 XX Synthetic.
 OS
 XX DE19937264-A1.
 PN XX PD 15-FEB-2001.
 XX XX 99DE-01037264.
 PF XX 06-AUG-1999; 99DE-01037264.
 PR XX 06-AUG-1999; 99DE-01037264.
 PA (DEFR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX PI Arndt M, Little M, Kipriyanov S, Krauss J, Pfreundschuh M;
 XX DR WPI; 2001-184000/19.
 DR N-PSDB; AAF6152.
 XX PT New Fv-antibody construct, useful for treating Hodgkin and Reed-Sternberg
 PT diseases, has binding sites for CD16 receptor and CD30 surface protein.
 XX PS Disclosure; Page 10; 18pp; German.

XX This invention describes a novel Fv-antibody construct (1) having binding sites for a CD16 receptor and a CD30 surface protein. The invention also describes (1) expression vector encoding (1); (2) transformants containing the vector of (1) by culturing cells of (1), and (2); and (4) kit comprising (1) and/or the vector of (1), and (2); and (4) such as buffers, solvents, carriers, controls and labels, or auxiliaries such as their replacements. The products of the invention have cytostatic activity. (1) causes lysis of CD30+, specifically tumor, cells. It activates natural killer cells, through the CD16 receptor, and directs them to CD30-expressing cells. (1) are used to treat diseases in which

CD50+ cells are implicated, particularly tumors and specifically than known or Reed-Sternberg diseases. (1) have a stronger lytic action than known bi-specific antibodies, can be produced on a large scale with high purity, and contain no components that can induce unwanted immune responses						
Query	Match	Score	DB	Length	DB	Score
QY	Query Match	100.0%	Score 1395;	DB 4;	Length 262;	
QY	Best Local Similarity	100.0%	Pred. No. 1	-e-94;		
QY	Mismatches	0;	Mismatches	0;	Indels	0;
QY	Matches	262;	Conservative	0;	Gaps	0
QY	Sequence	262 AA:	SO	XX	SO	XX
QY	MAQVOLQQSGLYLRPGTSVKSICKSASGIFTNTWLGWVQKRPQHGLEWIGDYPGGGTY	60	1	MAQVOLQQSGLYLRPGTSVKSICKSASGIFTNTWLGWVQKRPQHGLEWIGDYPGGGTY	60	
QY	1 NYNEKFKGKATVADTSSRTAYVQVRLSTEDSAYFCARSASMYFDWGMARTVTYSSA	120	61	1 NYNEKFKGKATVADTSSRTAYVQVRLSTEDSAYFCARSASMYFDWGMARTVTYSSA	120	
QY	61 NYNEKFKGKATVADTSSRTAYVQVRLSTEDSAYFCARSASMYFDWGMARTVTYSSA	120	61	NYNEKFKGKATVADTSSRTAYVQVRLSTEDSAYFCARSASMYFDWGMARTVTYSSA	120	
QY	121 KTPKLGGDIETLSPKEMSTSVDGRVNTYKASONVGTVNAWQKPCQSPKVLYSAS	180	121 KTPKLGGDIETLSPKEMSTSVDGRVNTYKASONVGTVNAWQKPCQSPKVLYSAS	180		
QY	121 KTPKLGGDIETLSPKEMSTSVDGRVNTYKASONVGTVNAWQKPCQSPKVLYSAS	180	121 KTPKLGGDIETLSPKEMSTSVDGRVNTYKASONVGTVNAWQKPCQSPKVLYSAS	180		
QY	181 YRYSGVPDRFTGSGGTDFLTISVQSEDLAETYFCQQYHTYPLTFGGGTKEIKRADA	240	181 YRYSGVPDRFTGSGGTDFLTISVQSEDLAETYFCQQYHTYPLTFGGGTKEIKRADA	240		
QY	181 YRYSGVPDRFTGSGGTDFLTISVQSEDLAETYFCQQYHTYPLTFGGGTKEIKRADA	240	181 YRYSGVPDRFTGSGGTDFLTISVQSEDLAETYFCQQYHTYPLTFGGGTKEIKRADA	240		
QY	AAGSEQKLISEEIDLNSHHHHHH	262	241 AAGSEQKLISEEIDLNSHHHHHH	262		
QY	AAGSEQKLISEEIDLNSHHHHHH	262	241 AAGSEQKLISEEIDLNSHHHHHH	262		

RESULT 2

ID ADE29202 standard; protein; 264 AA.
XXX

AC ADE29202;

DT 29-JAN-2004 (first entry)

Multivalent multimeric antibody CD19

xx multivalent multimeric antibody: his

KW human B cell marker; CD19; human Fcg^{RI}

KW B-cell mediated autoimmune disease;

KW murine.

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Introduction / Conclusion

Table 1. Mean FT by Region

Region FT 50 : .66

/label = Comprimentar

/label= Complimentar

/label= Synthetic list

ET
regier.
zur
/label=Complimentar

Region 180.: 186 /186: common

Table 1. Summary of the results of the regional analysis.

FT Region 247. .257

/taber/c-myc-epicope 259 : 264

/label= 6xHis_tag

PN EP1314741-A1.

QY 61 NYNEKFKGKATVADTSRATTAYVQVRSITSEDASVYFCARSAS-----WYP--DVGART 113
 Db 81 NYNGFKGKATLIADESSTAYMOLSSASEDASVYFCARRETTVGRYYANDYWGQT 140

QY 114 TVTYSSAKTTPKLGDEDIELTQSPEKFMSTSIVGDRYNTVYKASQNYTGNTAWFOOKPGQSPK 173
 Db 141 SVTYSSAKTTPKLGDEDIELTQSPEKFMSTSIVGDRYNTVYKASQNYTGNTAWFOOKPGQSPK 199

QY 174 LVIYASTRYSGVPPRFETSGSGCDFTLITISVQSEDLAFYFCOQHHTYPLTFGGCTLE 233
 Db 200 RWIYDTSKLASGVPAHFRGSGCTSYSLTSGMEADEDATYCCQWSNPTFGSGTLE 259

QY 234 IKRADAAAAGSEQKLISEEDLNSHHHHHH 262
 Db 260 INRADTAPSEQKLISEEDLNSHHHHHH 288

RESULT 7
 AAW82317 standard; protein; 288 AA.

XX AAW82317;
 AC XX
 DT 26-FEB-1999 (first entry)
 DE Mouse bispecific antibody variant OKT3/anti-CD19 protein.
 XX OKT3; monoclonal antibody; Mab; Point mutation; transplant rejection;
 KW organ recipient; diagnosis; tumour; therapy; diabody; anti-CD19;
 KW anti-CD3.
 XX Mus sp.
 OS Synthetic..
 OS Synthetic..
 XX DE19721700-C1.
 XX PD 19-NOV-1998.
 XX PF 23-MAY-1997; 97DE-01021700.
 XX PR 23-MAY-1997; 97DE-01021700.
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

XX Kipriyanov S, Little M, Moldenhauer G;
 PI WPI; 1998-596150/51.
 DR N-PSDB; AAV733331.
 DR Sequence 288 AA;

XX This sequence represents a protein which has anti-CD19 activity and is encoded by a monoclonal antibody (Mab) diabody derived from OKT3 with a point-mutation where Cys at position H100A is replaced with another polar amino acid, in this example Ser. The diabody encodes two OKT3 proteins, one which has anti-CD19 activity and one with anti-CD3 activity. The Mab is used in lowering or eliminating the transplant rejection in an organ recipient and for diagnostic methods for tumours and tumour therapy.

PS Disclosure; Fig 3; 8pp; German.
 XX This sequence represents a protein which has anti-CD19 activity and is encoded by a monoclonal antibody (Mab) diabody derived from OKT3 with a point-mutation where Cys at position H100A is replaced with another polar amino acid, in this example Ser. The diabody encodes two OKT3 proteins, one which has anti-CD19 activity and one with anti-CD3 activity. The Mab is used in lowering or eliminating the transplant rejection in an organ recipient and for diagnostic methods for tumours and tumour therapy.

SQ Sequence 288 AA;
 XX Score 936; DB 2; Length 288;

Query Match 67.1%; Best Local Similarity 69.0%; Matches 185; Conservative 23; Mismatches 54; Indels 6; Gaps 2;
 CC 1 MAQVOLQSGABELVRPETSVKISCKASGYTFNWLQWVKORPGGLEWIGDIYPCGGYT 60
 CC 21 MAQVQLQSGABELVRPETSVKISCKASGYTFNWLQWVKORPGGLEWIGYINPSRGYT 80

QY 61 NYNEKFKGKATVADTSRATTAYVQVRSITSEDASVYFCAR-SASYFDVGARTTVTVS 118
 Db 81 NYNCQFKDKATLITDKSSSTATMQSSLTSEDASVYCARRYDDHYSLDYWGQTTLV 140

RESULT 8
 AAW82316 standard; protein; 288 AA.

XX AAW82316;
 AC XX
 DT 26-FEB-1999 (first entry)
 DE Mouse OKT3 variant antibody protein.
 XX OKT3; monoclonal antibody; Mab; Point mutation; transplant rejection; KW organ recipient; diagnosis; tumour; therapy.
 XX Mus sp.
 OS Synthetic..
 XX PN DE19721700-C1.
 XX PD 19-NOV-1998.
 XX PF 23-MAY-1997; 97DE-01021700.
 XX PR 23-MAY-1997; 97DE-01021700.
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 XX PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PI Kipriyanov S, Little M, Moldenhauer G;
 XX WPI; 1998-596150/51.
 DR N-PSDB; AAV733335.

XX Monoclonal antibody OKT3 with point-mutation - where cysteine is replaced by another polar amino acid, useful for controlling transplant rejection, PT and in tumour diagnostics and therapy.
 XX Sequence 288 AA;
 PS Claim 3; Fig 2; 8pp; German.
 XX This sequence represents a monoclonal antibody (Mab) derived from OKT3 with a point-mutation where Cys at position H100A is replaced with another polar amino acid, in this example Ser. The Mab is used in lowering or eliminating the transplant rejection in an organ recipient, PT and in tumour diagnostics and therapy.

SQ Query Match 67.1%; Score 936; DB 2; Length 288;
 CC Best Local Similarity 69.0%; Pred. No. 1e-60; Matches 23; Mismatches 54; Indels 6; Gaps 2;
 CC Matches 185; Conservative 23; Mismatches 54; Indels 6; Gaps 2;
 CC 1 MAQVOLQSGABELVRPETSVKISCKASGYTFNWLQWVKORPGGLEWIGDIYPCGGYT 60
 CC 21 MAQVQLQSGABELVRPETSVKISCKASGYTFNWLQWVKORPGGLEWIGYINPSRGYT 80

QY 61 NYNEKFKGKATVADTSRATTAYVQVRSITSEDASVYFCAR-SASYFDVGARTTVTVS 118
 Db 81 NYNCQFKDKATLITDKSSSTATMQSSLTSEDASVYCARRYDDHYSLDYWGQTTLV 140

Db	81 NYNQKFKOKATLITDKSSSTAYMQLSISLTSEDASVYCCARYDDHYSIDYNGQGTTLTVS 140	Qy	115 VTVSSAKTTPKUGGDLIELTOSPKFMSTSVGDRVNTYKASQNVGTTVWFOOKPGQSPKV 174
Qy	119 SAKTTPKUGGDLIELTOSPKFMSTSVGDRVNTYKASQNV---GTINAWFQOKPGQSPKV 174	Db	393 VTVSSAKTTPKUGGDLIELTOSPKFMSTSVGDRVNTYKASQNVGTTVWFOOKPGQSPKV 451
Db	141 SAKTTPKUGGDLIELTOSPKFMSTSVGDRVNTYKASQNVGTTVWFOOKPGQSPKV 200	Qy	175 LIYASASYRSGVPDRFTSGSGTDFTLTLISNYQSEDLAEYFCQQHTYPLTFGGTKEI 234
Qy	175 LIYASASYRSGVPDRFTSGSGTDFTLTLISNYQSEDLAEYFCQQHTYPLTFGGTKEI 234	Db	452 WIYDTSKLASGYPAHFRGSGSTSYSITGMEAEATATYICQOVSNNPFFGSGTKEI 511
Db	201 LIYDASNLVG1PPRFSSSGTDFLNLHPCQSTEDPWTIFQQGTRKEI 260	Qy	235 KRADAAAAGSEQKLISEBDLNSHHHHH 262
Qy	235 KRADAAAAGSEQKLISEBDLNSHHHHH 262	Db	512 NRADTAFTGSEOKLISEBDLNSHHHHH 539
Db	261 KRADAAAAGSEQKLISEBDLNSHHHHH 288		
		RESULT 9	
		AAY50822	
ID	AAY50822 standard; protein; 554 AA.	ID	AAY50822 standard; protein; 554 AA.
XX		XX	
AC		AC	
XX		XX	
DT	18-FEB-2000 (first entry)	DT	18-FEB-2000 (first entry)
XX		XX	
DE	Fv-antibody construct containing antibody 9E10 epitope protein.	DE	Fv-antibody construct containing antibody 9E10 epitope protein.
XX		XX	
XX	Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;	XX	Multivalent; Fv-antibody; antiviral; antibacterial; cytostatic;
KW		KW	
KW	Diagnosis; therapy; disease.	KW	Diagnosis; therapy; disease.
XX		XX	
OS		OS	
Synthetic.		Synthetic.	
XX		XX	
PN	DE19819846-A1.	PN	DE19819846-A1.
XX		XX	
PD	11-NOV-1999.	PD	11-NOV-1999.
XX		XX	
PF	05-MAY-1998; 98DE-01019846.	PF	05-MAY-1998; 98DE-01019846.
XX		XX	
PR	05-MAY-1998; 98DE-01019846.	PR	05-MAY-1998; 98DE-01019846.
XX		XX	
PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.	PA	(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
XX		XX	
PA	DEUT KREBSFORSCHUNGSZENTRUM.	PA	DEUT KREBSFORSCHUNGSZENTRUM.
XX		XX	
PT	Little M, Kipriyanov S;	PT	Little M, Kipriyanov S;
XX		XX	
PR	WPI; 2000-024472/03.	PR	WPI; 2000-024472/03.
XX		XX	
DR	N-PSDB; AAZ3432.	DR	N-PSDB; AAZ3432.
XX		XX	
PR	Multivalent Fv-antibody constructs with at least four variable domains connected by 1, 2 and 3 peptide linkers.	PR	Multivalent Fv-antibody constructs with at least four variable domains connected by 1, 2 and 3 peptide linkers.
XX		XX	
PS	Example 1; Fig 6; 14pp; German.	PS	Example 1; Fig 5; 14pp; German.
XX		XX	
PS	Multivalent Fv-antibody constructs with at least four variable domains connected by 1, 2 and 3 peptide linkers.	PS	Multivalent Fv-antibody constructs with at least four variable domains connected by 1, 2 and 3 peptide linkers.
XX		XX	
PS	Example 1; Fig 6; 14pp; German.	PS	Example 1; Fig 5; 14pp; German.
XX		XX	
CC	This invention describes a novel multivalent Fv-antibody construct with at least four variable domains that are connected to one another by 1, 2 and 3 peptide linkers. The construct has antiviral, antibacterial and cytostatic activity. The multivalent Fv-antibody constructs are useful for the diagnosis and/or therapy of disease, especially viral, bacterial or tumor diseases. The multivalent Fv-antibody constructs have increased stability when in the form of a single chain dimer. This sequence represents a bivalent Fv antibody construct composed of the antibody 9E10 epitope in expression plasmid pDISC3x19-SU	CC	This invention describes a novel multivalent Fv-antibody construct with at least four variable domains that are connected to one another by 1, 2 and 3 peptide linkers. The construct has antiviral, antibacterial and cytostatic activity. The multivalent Fv-antibody constructs are useful for the diagnosis and/or therapy of disease, especially viral, bacterial or tumor diseases. The multivalent Fv-antibody constructs have increased stability when in the form of a single chain dimer. This sequence represents a bivalent Fv antibody construct composed of the antibody 9E10 epitope in expression plasmid pDISC3x19-SU
XX		XX	
SQ	Sequence 539 AA;	SQ	Sequence 554 AA;
Query Match	66.7%; Score 930; DB 3; Length 539;	Query Match	66.7%; Score 930; DB 3; Length 554;
Best Local Similarity	67.5%; Pred. No. 5.4e-60;	Best Local Similarity	67.5%; Pred. No. 5.4e-60;
Matches 181; Conservative	28; Mismatches 51; Indels 8; Gaps 3;	Matches 181; Conservative	28; Mismatches 51; Indels 8; Gaps 3;
Qy	2 AQVOLQSGAELVRPGTSVKSICKASGTTFTNTWLGMWTKQRPHGLEWIGDIYPGGYT 61	Qy	2 AQVOLQSGAELVRPGTSVKSICKASGTTFTNTWLGMWTKQRPHGLEWIGDIYPGGYT 61
Db	273 SQVLLQQSAELVRPGTSVKSICKASGTTFTNTWLGMWTKQRPHGLEWIGDIYPGGYT 332	Db	288 SQVOLQSGAELVRPGTSVKSICKASGTTFTNTWLGMWTKQRPHGLEWIGDIYPGGYT 347
Qy	62 YNEKFKGKATVTAATDSSRTAYVQVRLSTSEDSAYFCARSAS----WYF--DWFGARTT 114	Qy	62 YNEKFKGKATVTAATDSSRTAYVQVRLSTSEDSAYFCARSAS----WYF--DWFGARTT 114
Db	333 YNGKEFKGKATLTADESSTAYMQLSIAESDAYSFCARRETIVGRYYAMDYWQGQTS 392	Db	348 YNGKEFKGKATLTADESSTAYMQLSIAESDAYSFCARRETIVGRYYAMDYWQGQTS 407

QY 115 VTVSSAKTPKLGGDIELTQSPKEMSTSVGDRVNTVYKASQNYGTNVAFQOKPGQS PKV 174
 DB 408 VTVSSAKTPKLGGDIELTQSPKEMSTSVGDRVNTVYKASQNYGTNVAFQOKPGQS PKV 466
 QY 175 LIYSASYRVSGVDPRTGSGTDFTLTLISVNOSEDLLAEYFCOOYHTYPLTFCGGTKLBI 234
 DB 467 WIDTSKLASGVPAHFRSGSGTYSLISGMERADAATYCCQWSNPPTFGSGTKLBI 526
 QY 235 KRDAAAANGSEQLISEEDLNLSHHHHH 262
 DB 527 NRADTAARTSSEQKLISEEDLNLSHHHHH 554

RESULT 11
 ADR28054 standard; protein; 269 AA.
 ID ADR28054 ;
 XX AC ADR28054 ;
 XX DT 07-OCT-2004 (first entry)
 DB NPB polypeptide scFv1, seq id 1.
 XX CYostatic; metastasis inhibitor; neuropilin binder; NPB; scFv;
 KW single chain antibody; neuropilin-1; NP-1; angiogenesis; tumour; cancer.
 XX OS Mus sp.
 OS Synthetic.
 XX EH
 FT Location/Qualifiers
 FT /note= "complementary determining region claimed under
 FT claim 5"
 XX WO2004056874-A2.
 PN XX
 PD 08-TUL-2004.
 XX PP 22-DEC-2003; 2003WO-EP014756.
 XX PR 20-DEC-2002; 2002US-0435893P.
 PR 15-JAN-2003; 2003EP-000000615.
 XX PA (XERI-) XERION PHARM AG.
 PA (TUFT) UNIV TUFTS.
 XX Unger CM, Beste G, Zehetmeier C, Lain B, Torella C, Niewohner J,
 PI Jay DG, Bustace BK, Knauer R, Jensen KH,
 XX DR WPI; 2004-0507700/48.
 DR N-PSDB, ADR28056.
 PS XX
 CC The invention relates to a neuropilin binder (NPB) (I) which is a polypeptide, antibody, scFv, antibody fragment or bioconjugate, that modulates neuropilin-1 function or inhibits NP-1 dependent angiogenesis of endothelial cells and/or invasion of tumor cells useful for treating cancer.
 CC
 PT Claim 2: SEQ ID NO 1; 120pp; English.
 PT
 CC The invention relates to a neuropilin binder (NPB) (I) which is a polypeptide, antibody, scFv, antibody fragment or bioconjugate, that modulates neuropilin-1 (NP-1) function or inhibits NP-1 dependent angiogenesis of endothelial cells and/or invasion of tumor cells, whereby the NPB binds to NP-1 and modulates NP-1 function. Further disclosed is an ex vivo method of determining the dependency of the invasiveness of a naturally occurring invasive cancer cell on the functionality of NP-1. The NPB of the invention is an inhibitor of metastasis of NP-1 mediated invasion and/or adhesion and an inhibitor of tumor-associated NP-1 dependent angiogenesis. The NPB of the invention is useful for detecting NP-1 expression, modulation of NP-1 function, particularly modulation or inhibition of NP-dependent invasion or adhesion of cells, preferably tumour cells. It is useful in the manufacture of medicament for the treatment or prevention of NP-dependent

CC angiogenesis and non-physiological blood vessel growth, particularly correlated with a tumour. It is also useful for treatment or prevention of cancer and/or metastasis of tumour cells. The current sequence represents a single chain antibody neuropilin binder (NPB) polypeptide.

XX SQ Sequence 269 AA;

Query	Match	65.9%	Score 919.5;	DB 8;	Length 269;
Best Local Similarity	73.6%;	Pred. No. 1.5e-59;			
Matches	184;	Conservative	17;	Mismatches	36;
				Indels	13;
				Gaps	3;

QY 3 QYQQQSAELVRPGTSVYKISKAQSGTFTNNWGLWYKORPHGLEWIGDIYPOGGTYN 62.
 Db 1 EVQLQQSGPELVKPGALVKISKAQSGTFTSIDNWYKORPGQGLEWIGWIYCDGSIKY 60

QY 63 NEKEFKGRATVYTAUTSRTAYVQTRSLTEBDAYVFCARSASWYPTDWGARTTVVSSAKT 122
 Db 61 NEKEFKGRATLTVQDLSSTTVQMQLSLSITSENAYFCARGK-YFDYNGQGTITLTGSTGG 119

QY 123 TPKIGG-----DIELTQSPKFMSTSVPGRVNTVYKASQNYGTNVAFQOKPGQS PKV 174
 Db 120 GS CGCGSGCGGSA LDIVMTQSPKFMSTSVPGRVNTVYKASQNYGTNVAFQOKPGQS PKV 179

QY 175 LYASASYRVSGVDPRTGSGTDFTLTLISVNOSEDLEYFCOOYHTYPLTFCGGTKLBI 234
 Db 180 LYASASFSSGVPRFTGSGTDFTLTLISVNOSEDLEYFCOOYNSYPTFGGTKLBI 239

QY 235 KRA DAAAAGS 244
 Db 240 K----AAAGA 245

RESULT 12
 ADFP5426
 ID ADFP5426 standard; protein; 283 AA.
 XX AC ADFP5426 ;
 XX DT 26-FEB-2004 (first entry)
 XX DB V122scFv clone.
 XX KW Fv library.
 XX OS Unidentified.
 XX PN JP2003334075-A.
 XX PD 25-NOV-2003.
 XX PF 21-MAY-2002; 2002JP-00145858.
 XX PR 21-MAY-2002; 2002JP-00145858.
 XX PA (NISB) JAPAN TOBACCO INC.
 XX DR WPI; 2004-027982/03.
 XX N-PSDB; ADF85425.

XX Mutated Fv library useful for screening mutated Fv for preparation of antibodies having mutations at specific positions. The present invention relates to mutated Fv library having mutations at position k (k is integer 2 ≤ k ≤ m) designed such that the amino acid at position k (m is integer 2 ≤ m; k &neq; 20) is introduced at amino acid position m (m is integer 2 ≤ m; (n-1) is integer 3 ≤ n ≤ m) chosen from a region consisting of n residues contained in complementarity determining regions (CDR) or other closer regions of an antibody, and forms limited Fv repertoire. The invention can be used for efficiently acquiring mutated antibody. The present sequence represents V122scFv clone.

XX	Sequence 283 AA;	CC intra- or extracellular domain of the poliovirus receptor (PVR) - also known as CP155 (cluster of differentiation 155). The molecules of the invention have the ability to modulate receptor mediated adhesion, trafficking and/or invasion behaviour of a cell expressing PVR. The molecules of the invention are useful for the prevention and/or treatment of proliferative disorders, cancer or metastasis. The molecules of the invention are also useful for identifying agents that can modulate PVR-mediated adhesion or invasion potential of cells. The present amino acid sequence represents a PVR-specific scFv protein of the invention.
SQ	Query Match Similarity 65.8%; Pred. No. 2, 2e-59; Best Local Similarity 69.4%; Matches 186; Conservative 21; Mismatches 50; Indels 11; Gaps 3;	XX
Qy	1 MAQVQLQSGAELYVRPGTSVKLISKASGYTFTNWLGMVKORPGHGLEWIGDLYPGGGYT 60	XX
Db	2 21 MAQVQLQSGAELYVRPGTSVKLISKASGYTFTNWLGMVKORPGHGLEWIGDLYPGGGYT 60	XX
Qy	61 NYNEKFCKATYADTSRTAYQVSRLTSEDAVYFCARSASWYFDWIGARTTVYSA 120	Sequence 267 AA;
Db	81 NYNEKFCKATYADTSRSLTSDSSTAYMELSSLTSDSAAVYCAKKG--LDYWGOCTTVYSG 137	Query Match Similarity 65.3%; Score 911.5; DB 8; Length 267; Best Local Similarity 72.8%; Pred. No. 5.8e-59; Mismatches 19; Indels 17; Gaps 4; Matches 182; Conservative 32; Mismatches 32;
Qy	121 KTPBKLG-----DIEUTQSPKEMSTVGDRTNVTYKASQNGTNVAWFOQKPGQSKV 174	Qy 5 OLOQSGAELVLRPGTSVKISCKASGTYPTFTNYWLGMVKORPGHGLEWIGDLYPGGGYTNE 64
Db	138 GGASGGGGGGGGSDIELTQSPKEMSTVGDRTSCKASQFTGTTVWYQXPQGSPKA 197	Db 1 QLOQSGPBLVKQASVSKCKTSGYTTEYTMHWKOSHGSLEWIGGHPNGDTSYNQ 60
Qy	175 LIYSASYRVSGVPDRFTSGSGTDFTLTISNVQSEDIALEYFCOOHTYPLTFFGGTKEI 234	Qy 65 KPKGKATITADTSRPTAVQVSRLTSEDAVYFCARSASWY-FDYGARTTVYSSAKT 122
Db	198 LIYSASTRPTGVDRFTSGSGTDFTLTISNVQSEDIALEYFCOOHTYPLTFFGGTKEI 257	Db 61 RPKGKATITDVDESSSTAYMELRSLTSEDAVYFCARSASWY-FDYGARTTVYSSAKT 122
Qy	235 KRADAAGASEQKLISEEDLNSTHHHH 262	Qy 123 TPKLGG-----DIBLTQSPKEMSTVGDRTVNTYKASQNGTNVAWFOQKPGQSPKV 174
Db	258 KRAAGAPVPPVPPDL--BPERAAHHHHHH 283	Db 118 GSQGGSSCGGGGSALIDMTQSPKEMSTVGDRTVICKASQNVGTNAWYQOKPGQSPKA 177
RESULT 13		Qy 175 LIYSASYRVSGVPDRFTSGSGTDFTLTISNVQSEDIALEYFCOOHTYPLTFFGGTKEI 234
ADR70320	ID ADR70320 standard; protein; 267 AA.	Db 178 LIYSASYRVSGVPDRFTSGSGTDFTLTISNVQSEDIALEYFCOOHTYPLTFFGGTKEI 237
AC	ADR70320;	Qy 235 KRADAAGASEQKLISEEDLNSTHHHH 244
XX	DT 18-NOV-2004 (first entry)	Db 238 K---AIAGA 243
DB	Poliovirus receptor (PVR)-specific scFv2 protein.	RESULT 14
XX	poliovirus receptor; PVR; CD155; Cluster of differentiation 155;	ADP84954
KW	receptor mediated adhesion modulation;	ID ADP84954 standard; protein; 267 AA.
KW	cell trafficking behaviour modulation;	XX
KW	cell invasion behaviour modulation; Proliferative disorder; cancer;	AC ADP84954;
KW	metastasis; PVR-mediated adhesion; PVR-mediated invasion potential;	XX
KW	scFv2.	DT 09-SEP-2004 (first entry)
OS	Unidentified.	XX
XX	Single chain Fv fragment SEQ ID NO 96.	DE
PN	WO2004074324-A2.	XX
XX	antibody; Core-1 antigen; framework region; immunoglobulin superfamily;	KW
XX	protease inhibitor; lectin; helix-bundle protein; lipocalin;	KW
XX	cell	KW
XX	variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;	KW
XX	alleviation; treatment; tumour; breast; colon; stomach; pancreas;	KW
XX	large/small intestine; ovary; cervix; lung; prostate; kidney; liver;	KW
XX	metastasis.	KW
XX	Unidentified.	OS
PA	WO2004050707-A2.	XX
PA	antibody; Core-1 antigen; framework region; immunoglobulin superfamily;	XX
(TUFT) UNIV TUFTS.	protease inhibitor; lectin; helix-bundle protein; lipocalin;	KW
XX	cell	KW
XX	variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;	KW
XX	alleviation; treatment; tumour; breast; colon; stomach; pancreas;	KW
XX	large/small intestine; ovary; cervix; lung; prostate; kidney; liver;	KW
XX	metastasis.	KW
PR	19-FEB-2004; 2004WO-EP001637.	XX
PR	24-FEB-2003; 2003US-0450064P.	XX
PR	28-MAY-2003; 2003EP-00012314.	XX
XX	WPI; 2004-652917/63.	PR 29-NOV-2002; 2002DE-01056300.
DR	N-PSDB; ADR70322.	XX
XX	New molecules that modulate poliovirus receptor (PVR) mediated adhesion, trafficking and/or invasion behavior of a cell expressing CD155 or PVR, useful for preventing or treating proliferative disorders, such as cancer.	PR 17-JUN-2004.
XX	New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens,	XX
PS	Claim 7; SEQ ID NO 4; 87pp; English.	XX
XX	The invention comprises molecules that specifically bind to at least one	XX
CC	(NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.	CC
PI	Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;	PI
PI	Christensen PA;	PI
DR	WPI; 2004-411095/43.	DR
XX	New recognition molecules, e.g. antibodies (and nucleic acids) that bind specifically to Core-1 antigens,	PT

PT prevention of tumors and metastases.
 XX Claim 26; SEQ ID NO 96; 136pp; German.
 XX
 CC This invention describes novel recognition molecules, especially antibodies that bind specifically to the Core-1 antigen. The recognition molecules are used to make constructs containing the framework regions that separate, include and/or flank the specified domains, especially where the framework regions are from the immunoglobulin (Ig) superfamily.
 CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.
 CC Most especially the framework regions are from antibodies, particularly the variable heavy chain (VH) and the variable light chain (VL) of human and/or murine origin. The constructs may also include a His or myc tag, a lysine-rich region and/or a multimerisation domain, most particularly it is a single-chain antibody fragment, multibody, Fab fragment, fusion protein of an antibody fragment with peptide or protein, and/or an Ig of types G, M, A, E or D and/or their subclasses. It may be human, humanised, murine or chimeric, e.g. IgM without the J chain. The additional sequences/structures in the constructs are Ig domains of various species, interacting or stabilising domains, signal sequences, fluorescent dyes, toxins, antibodies with catalytic activity or other specificities, cytolytic agents, enzymes, immuno-modulators or effectors, MHC molecules, antigens, chelators for radioactive labels, liposomes, transmembrane domains, viruses and/or cells, specifically macrophages. The antibodies, also constructs containing them, nucleic acid encoding them, and related vectors and host cells, are useful for prevention (e.g. as vaccine), diagnosis, alleviation, treatment, monitoring and/or secondary treatment of tumours (specifically of breast, colon, stomach, pancreas, large/small intestine, ovary, cervix, lung, prostate, kidney and/or liver) and/or metastases (particularly to liver), specifically where these are positive for the C1 antigen. The products of the invention provide simple, reliable and efficient detection of tumours. They are specific for carcinoma and show almost no binding to healthy tissue.
 XX Sequence 267 AA;

Query Match 65.2%; Score 909.5; DB 8; Length 267;
 Best Local Similarity 66.5%; Pred. No. 8.1e-59; Indels 21; Gaps 4;
 Matches 179; Conservative 29; Nsmatches 40; Delins 21; Gaps 4;
 QY 3 QVQLOQGAELVRPGTSVKISCKASGTYTFTNYLGWVKQRPHGLEWIGDIPGGYTNY 62
 1 QVQKESGAELVRPGTSVKISCKASGTYTFTNYLGWVKQRPHGLEWIGDIPGGYTNY 60
 DB 63 NEKFKGKATVADTSRSTAVQVRLTSSEANTCARSASWYDVS----WGRARRY 115
 1 NEKFKGKATLTADTSSTAVQQLSSTSSEASVFCAT----YDAAGPGEAYNGQGRTY 115
 QY 116 TVSSAKTPKLGGDIBLTQSPKFMSTSVDGRVNNTYKASONV----GTNVAWFQKPGQ 170
 DB 116 TVSSASSGSGSADIQMTQPLSLPVSLGDOAISRSSSIVHSNGNTYLEWLQKPGQ 175
 QY 171 SPKVLIYASTRYSGYPDRFGSGSCTDFLTISVYQSEDLAEYFCQOYHTYPLTFGGST 230
 DB 176 SPKLIIYKVSNRGYPDRFGSGSCTDFLKISRVEAEDLGVYCFQGSHPVTFGGST 235
 QY 231 KLEIKRADA---AAGSEQKQLISEEDLN 255
 DB 236 KLEIKRADAHHHHHHGAAEQLISEEDLN 264
 SQ Sequence 264 AA;

Query Match 64.9%; Score 906; DB 8; Length 264;
 Best Local Similarity 66.5%; Pred. No. 1.5e-58; Indels 24; Gaps 5;
 Matches 179; Conservative 30; Nsmatches 36; Delins 24; Gaps 5;
 QY 3 QVQLOQGAELVRPGTSVKISCKASGTYTFTNYLGWVKQRPHGLEWIGDIPGGYTNY 62
 1 QVQKESGAELVRPGTSVKISCKASGTYTFTNYLGWVKQRPHGLEWIGDIPGGYTNY 60
 DB 63 NEKFKGKATVADTSRSTAVQVRLTSSEANTCARSASWYDVS----WGRARRY 115
 QY 63 NEKFKGKATLTADTSSTAVQQLSSTSSEASVFCAT----YDAAGPGEAYNGQGRTY 115
 DB 61 NEKFKGKATLTADTSSTAVQQLSSTSSEASVFCAT----YDAAGPGEAYNGQGRTY 115

Qy	116	TVSSAKTTPKGGLIEETOSPKMESTSGDRNNTYKASQNV---	-GTVNAPWQXPQGQ	170
Dbb	116	TVSSASSS--SAIDIQMTOPPLSPVSDQASISSCSQSVHNSNENTLEYWLXPKPGQ	172	
Qy	171	SPKVLISSASYRSGVPDFGSGGTDFTLISNVQSEDIAEYFCQQHTYPLTFGGGT	230	
Dbb	173	SPKLIIKYVSNRFFGVPDFGSQGDTFLKISRVAEDLGYYCFQGSHVPYTFGGGT	232	
Qy	231	KLEIKRADA--AAGSEQKLISEEDIN	255	
Dbb	233	KLEIKRAAAHHHHHHGAAEQKLISEEDIN	261	

Search completed: February 9, 2006, 03:27:46
Job time : 275.825 secs

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GenCore version 5.1.7

OM protein - protein search, using SW model

Run on: February 9, 2006, 03:28:13 ; Search time 25.4654 Seconds

(without alignments)

989.922 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQVQLQSGAELVRGTSV.....GSEQKLISEEDLNSHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR_80;*

1: pir;:*

2: pir;:*

3: pir;:*

4: pir;:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	708	50.8	268	2 A56446	Ig heavy chain V r
2	664.5	47.6	249	2 S41374	single chain Fv, an Ig heavy chain pre
3	520.5	41.8	233	2 JC5322	specific singl Ig heavy chain V r
4	520.5	37.3	141	2 A39276	Ig heavy chain V r
5	516	37.0	121	1 GVMS11	Ig heavy chain V r
6	501	35.9	115	2 A56700	Ig heavy chain (an Ig gamma chain - m
7	497	35.6	246	2 S38950	Ig gamma-2a chain
8	497	35.6	446	2 S40295	Ig kappa chain V r
9	496	35.6	107	2 A28195	Ig lambda chain V r
10	489	35.1	128	2 A47159	Ig heavy chain V r
11	486	34.8	119	2 PL0089	Ig heavy chain pre
12	486	34.8	136	2 PL0208	Ig heavy chain V r
13	484	34.7	123	2 B30560	Ig heavy chain V r
14	482	34.6	119	2 PL0086	Ig kappa chain V r
15	480	34.4	107	2 B28195	anti-DNA autoantib
16	478	34.3	108	2 PL0204	Ig heavy chain V r
17	476	34.1	119	2 PL0085	Ig heavy chain V r
18	475	34.1	140	2 PH1482	Ig heavy chain V r
19	472	33.8	117	2 S42466	Ig kappa chain V r
20	471.5	33.8	116	2 S53751	antibody Fab Jel 1
21	468.5	33.6	214	2 PC4202	monoclonal antibody
22	468	33.5	118	2 S38565	Ig heavy chain V r
23	468	33.5	119	2 C30562	Ig heavy chain V r
24	467.5	33.5	108	2 B44371	Ig kappa chain V r
25	467	33.5	138	2 F32513	Ig heavy chain pre
26	467	33.5	140	2 T01407	Ig heavy chain (my
27	466	33.4	119	2 B30562	Ig heavy chain V r
28	464.5	33.3	169	2 S37483	Ig gamma-2a chain
29	464	33.3	117	1 NMMS4E	Ig heavy chain V r

ALIGNMENTS

RESULT 1						
A56446	Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)	C;Species: Mus musculus (house mouse)	C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996	C;Accession: A56446	R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.	J. Biol. Chem. 270: 7829-7835, 1995
					A;Title: A high affinity dioxin-binding protein displayed on M13 is functionally identical	
					A;Reference number: A56446; PMID:952220583; PMID:7713873	
					A;Accession: A56446	
					A;Status: preliminary	
					A;Molecule type: mRNA	
					A;Cross-references: UNIPARC:UPI00001766D0; GB:U0617	
					C;Keywords: heterotetramer; immunoglobulin	
Query	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Match	50.8%	Score	708;	DB 2; Length 268;
Qy	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Best Local Similarity	54.3%	Pred. No.	2e-44;	Gaps 5;
Db	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Matches	146; Conservative	Mismatches	64;	Indels 18;
Qy	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Query	1	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	60	
Db	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Db	1	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	60	
Qy	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Qy	61	NYNEKPKGKATVTDSSRTAYVQVRLTSEDSAVYFCARSASYWYF---DVGKARTTVT	116	
Db	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Db	61	KYDPKFQGKATIAADTSSNTAYLQLISSLTSEDTAVYYC---ASVYLTRYENYRGCTTVT	117	
Qy	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Qy	117	VSS----AKTPPKGGDIELTQSPKEMSTSVDGRVNVTYKASSONGNVINAVWFQOKPGQ	170	
Db	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Db	118	VSSGGGGGGGGGGSDTELTQSPATMSASLGKEKVTMSGRASSYVNF-IYWWYQOKSDA	176	
Qy	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Qy	171	SPKVLIYASASRYRSGYVPDRFTGS3GTDFTLTISVQSEDALEYFQCOQVTHYPLTFGGGT	230	
Db	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Db	177	SPKLVYYTSHLPPEVPAKSGSGNSLTISMEGEDAATYRCQQFTSPPFGSGT	236	
Qy	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Qy	231	KLEIKRADA---AAAGSEOKLISBEDLN 255		
Db	MAQYOLQQSGAELVRPGTSVKSCKASGTYIFTNYWLGHYKQRPHGLEWTGDIYPGGGT	Db	237	KLEIKRSAAHHHHHGAAEQKLISBEDLN 265		

RESULT 2

Single chain Fv antibody - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C;Accession: S41374

R;Artsenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A;Description: Construction and functional characterization of a single chain Fv antibody

A;Reference number: S41374

A; Accession: S41374
 A; Status: Preliminary
 A; Molecule type: DNA
 A; Residues: 1-249 <ART>

A; Cross-references: UNIPARC:UPI000017C74A; EMBL:Z29480

Query Match 47.6%; Score 664.5; DB 2; Length 249;
 Best Local Similarity 54.8%; Pred. No. 2.7e-41; Indels 13; Gaps 3;
 Matches 136; Conservative 37; Mismatches 62; A; Status: Preliminary
 A; Molecule type: mRNA
 A; Residues: 1-141 <RPL>

Qy 3 QVQLQSGAELVRPGTSVKISCKASGTYFTNYWLGWYKORPGHGLEWIDYPGGTYN 62
 Db 1 QVQLQSGAELVRPGASTLCLSTCAAGFKDIDDHYWYKORPEKLENARTAPASGNKVY 60
 Qy 63 NEKFRKGKATVADTSSRAYVQRSLISAVFCAKASWFDV--WGAETPTVTS 120
 Db 61 VPRFQDKATITADTSSNAYLSSLISBDTAVYCARDTLYTSLGWGQSSTVTS 120
 Qy 121 KTPPKLGG -----DIELTQSPKFMSTSVDGRNVTYKASQNY-----GTNYAWFQQRPG 169
 Db 121 GGSGGGGGGGGGGGSDIEIQTSPSPSVVVPGESTSISCRSSSKSLLYSDODSYLFWFQRG 180
 Qy 170 QSPKVLIYASASYRGVPDRFTGSGSCDDFTLTISVQSEDALAEYFCQQHTYPLTFGGG 229
 Db 181 QSPKLIVRMSNLASGVDPDRFGSGSGTSFTRISVRAEDGVYYCNQHREXPFTGAG 240
 Qy 230 TKELEKRA 237
 Db 241 TKELEKRA 248

RESULT 3

JCS322
 P53 specific single-chain antibody Pab421 - human
 C; Species: Homo sapiens (man)
 C; Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
 C; Accession: JC5322
 R; Jannöt, C. B.; Hynes, N. E.
 Biochem. Biophys. Res. Commun. 230, 242-246, 1997
 A; Title: Characterization of scby-4-421, a single-chain antibody targeted to p53.
 A; Reference number: JCS322; MUID:90168950; PMID:9016757
 A; Accession: JC5322
 A; Molecule type: mRNA
 A; Residues: 1-233 <JAN>
 A; Cross-references: UNIPARC:UPI000017C2DE

A; Experimental source: hybridoma cell
 C; Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 41.8%; Score 533.5; DB 2; Length 233;
 Best Local Similarity 52.7%; Pred. No. 1.9e-35; Indels 17; Gaps 5;
 Matches 126; Conservative 30; Mismatches 66; A; Status: erratum
 A; Molecule type: mRNA
 A; Residues: 1-121 <Z42>

Qy 7 QOSGAELVRPGTSVKISCKASGTYFTNYWLGWYKORPGHGLEWIDYPGGTYN 66
 Db 1 QESGAELRSGASTLCLSTCAAGFKDIDDHYWYKORPEKLENARTAPASGNKVY 60

Qy 67 KGKATVADTSSRAYVQRSLISAVFCAKASWFDGARPTVTVSS 120
 Db 61 GVKATMADTSSNAYLSSLISBDTAVYCARDTLYTSLGWGQSSTVTS 116

Qy 121 KTPPKLGGDIELTQSPKFMSTSVDGRNVTYKASQNYTN 176
 Db 117 RASEGGSDIELTQSPKFMSTSVDGRNVTYKASQNYTN 176

Qy 177 YSASYRYSGVPDRFTGS3GTDFTLTISVQSEDALAEYFCQQHTYPLTFG-GGTKEI 234
 Db 177 YLVNSLESGVPARFSGSGTDFTLNIHREEDATYCQ-HIRELTSBEGTKLEI 233

Qy 230 TKELEKRA 237
 Db 241 TKELEKRA 248

RESULT 5

GWS11
 Ig heavy chain V region (MPC 11) - mouse
 C; Species: Mus musculus (house mouse)
 C; Date: 31-Oct-1980 #sequence_revision 29-Jun-1981 #text_change 09-Jul-2004
 C; Accession: A93708; A93711; A02027
 R; Zukut, R.; Cohen, J.; Givon, D.
 Nucleic Acids Res. 8, 3591-3601, 1980
 A; Title: Cloning and sequence of the cDNA corresponding to the variable region of immunoglobulin
 A; Reference number: A93708; MUID:81053741; PMID:6233904
 A; Accession: A93708
 A; Molecule type: mRNA
 A; Residues: 1-81; 'D' 93-103; 'GD' 106-121 <ZAK>
 A; Cross-references: UNIPROT:POL145; UNIPARC:UPI000017372D

A; Note: this sequence was translated from an mRNA isolated from a myeloma that secretes
 R; Zukut, R.; Cohen, J.; Givon, D.
 Nucleic Acids Res. 8, 4839-4840, 1980
 A; Reference number: A93711
 A; Content: erratum
 A; Accession: A93711
 A; Molecule type: mRNA
 A; Residues: 1-121 <Z42>

C; Superfamily: immunoglobulin V region; immunoglobulin homology
 F; 15-98: Domain: immunoglobulin homology <IMM>

Query Match 37.0%; Score 516; DB 1; Length 121;
 Best Local Similarity 77.7%; Pred. No. 7.3e-31; Mismatches 10; Indels 4; Gaps 1;

Qy 3 QVQLQSGAELVRPGTSVKISCKASGTYFTNYWLGWYKORPGHGLEWIDYPGGTYN 62
 Db 1 EAQLQSGAELVRPGTSVKISCKASGTYFTNYWLGWYKORPGHGLEWIDYPGGTYN 60

Qy 63 NEKFKGKATVADTSSRAYVQRSLISAVFCAKASWFDGARPTVTVSS 118
 Db 61 NDNLKGKATVADTSSRAYVQRSLISAVFCAKASWFDGARPTVTVSS 120

Qy 119 S 119

RESULT 4

A39276
 Ig heavy chain precursor V-D-J region (6-19) - mouse
 C; Species: Mus musculus (house mouse)

A;Accession: A28195
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI0000114D69; GB:M19766; NID:gi197039; PIDN:AAA38891.1; PMID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>

Query Match Score 436; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 1..8e-29;
Matches 95; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 129 DIELTQSDFKFMSTSVGDRVNTYKASQNGTNYAWFOQPGSPKVLIYSASYRSGVPD 188
Db 1 DILMTQSDFKFMSTSVGDRVNTYKASQNGTNYAWFOQPGSPKVLIYSASYRSGVPD 60

RESULT 12

PL0208 Ig heavy chain precursor V region anti-idiotypic antibody E225 - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 13-Feb-1998
C;Accession: PL0208
R;Souchon, H.; Doyen, N.; Riottot, M.M.; Rougeon, F.; Poljak, R.J.
Mol. Immunol. 27; 429-433; 1990
A;Title: Nucleotide sequence of the VH, VL regions of an anti-idiotypic antibody reactin
A;Reference number: PMID:1973259
A;Accession: PL0208
A;Molecule type: mRNA
A;Residues: 1-136 <SOU>
A;Cross-references: UNIPARC:UPI0000176C6P
A;Experimental source: hybridoma cell E225
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-19/Domain: signal sequence #status predicted <SIG>
F;34-117/Domain: immunoglobulin homology <IMM>
F;50-54/Region: complementarity-determining 1
F;69-85/Region: complementarity-determining 2
F;118-121/Region: complementarity-determining 3
F;122-136/Region: JH region

Query Match Score 486; DB 2; Length 136;
Best Local Similarity 74.6%; Pred. No. 1..3e-26;
Matches 88; Conservative 14; Mismatches 16; Indels 0; Gaps 0;

Qy 2 AVOVLOOGAELVYRPGRTSVKISCKASGYTFTNYWLGWVQKRPCHGLEWIGDIYPGGYTNY 61
Db 19 SVQQLQQGSENLVRGASVKAUSCKASGYTFTNYWLGWVQKRPCHGLEWIGDIYPGGYTNY 78

RESULT 13

B30560 Ig heavy chain V region (28.4.10A) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: B30560
R;Matanda, T.; Kabat, E.A.
J. Immunol. 142; 863-870; 1989
A;Title: Variable region cDNA sequences and antigen binding specificity of mouse monoclonal antibodies
A;Reference number: A30560; PMID:89110062; PMID:2464028
A;Accession: B30560
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-123 <MAT>
A;Cross-references: UNIPARC:UPI0000114E20; GB:M24269; NID:gi195619; PIDN:AAA38373.1; PMID:
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>

Query Match Score 484; DB 2; Length 123;

Best Local Similarity	77.2%	Pred. No.	1.6e-28;	Db	1 DILMTQSQKFMSTSVDRTSVTCKASQVNQNNVVAHQKPGSPKALIYSASYRSGVPD 60
Matches	95;	Conservative	7;	Mismatches	15;
Qy	3 QVOLQSGAELVRPCTSKISCKASGYTFINYLGWVORPGLEWIDIVGGGTNY 62	Indels	6;	Gaps	1;
Db	1 QVOLQSGAELVRPCTSKISCKASGYTFINYLGWVORPGLEWIDIVGGGTNY 60				
Qy	63 NEKPKGKATVTDTSRATAYQVRSLSITSDSAVFCARSAS-----WYFDWIGARTVT 116				
Db	61 NEKPKGKATLTDKSSTAYMQLSSSTAYMQLSSITSDSAVFCARSSPYDYGMWFDWIGAGTVT 120				
Qy	117 VSS 119				
Db	121 VSS 123				
<hr/>					
RESULT 14					
PL0086	Ig heavy chain V region (E4) - mouse				
C;Species:	Mus musculus (house mouse)				
C;Date:	07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 23-Jul-1999				
C;Accession:	PL0086				
R; /Week:	K.; Hasemann, C.; Pollok, B.; Alkan, S.S.; Brait, M.; Slacou, M.; Urbain, J.; Ca				
J; Exp. Med.:	169, 519-533, 1989				
A;Title:	Structural characterization of antiidiotypic antibodies; evidence that Ab2s are				
A;Reference number:	PL0080; MUID:89094248; PMID:2492056				
A;Accession:	PL0086				
A;Molecule type:	mRNA				
A;Residues:	1-119 <MEIE>				
A;Cross-references:	UNIPARC:UPI0000115F1F; GB:X58585; GB:Y00794; NID:951561; PIDN:CAA414				
A;Experimental source:	strain BALB/C				
C;Superfamily:	immunoglobulin V region; immunoglobulin homology				
C;Keywords:	heterotetramer; immunoglobulin F; 15-98; domain: immunoglobulin homology <IMM>				
Query Match	34.6% ; Score 482; DB 2; Length 119;				
Best Local Similarity	75.6% ; Pred. No. 2.1e-28;				
Matches	90; Conservative 8; Mismatches 19; Indels 2; Gaps 1;				
Qy	3 QVOLQSGAELVRPCTSKISCKASGYTFINYLGWVORPGLEWIDIVGGGTNY 62				
Db	1 QVOLQSGAELVRPCTSKISCKASGYTFINYLGWVORPGLEWIDIVGGGTNY 60				
Qy	63 NEKPKGKATVTDTSRATAYQVRSLSITSDSAVFCARSAS-----WYFDWIGARTVT 119				
Db	61 NEKPKGKATLTDKSSTAYMQLSSITSDSAVFCARSSPYDYGMWFDWIGAGTVT 119				
<hr/>					
RESULT 15					
B28195	Ig kappa chain V region (anti-haloperidol antibody B) - mouse				
C;Species:	Mus musculus (house mouse)				
C;Date:	01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Jan-2000				
C;Accession:	B28195				
R;Sherman, M.A.; Deans, R.J.; Bolger, M.B.					
J; Biol. Chem.:	263, 4059-4063, 1988				
A;Title:	Haloperidol binding to monoclonal antibodies. Hypervariable region amino acid s				
A;Reference number:	A28195; MUID:88153717; PMID:3267217				
A;Accession:	B28195				
A;Molecule type:	mRNA				
A;Residues:	1-107 <SHE>				
A;Cross-references:	UNIPARC:UPI0000114D6A; EMBL:M19767; NID:9197041; PIDN:AAA18892.1; PI				
C;Superfamily:	immunoglobulin V region; immunoglobulin homology				
C;Keywords:	heterotetramer; immunoglobulin F; 16-90; domain: immunoglobulin homology <IMM>				
Query Match	34.4% ; Score 480; DB 2; Length 107;				
Best Local Similarity	86.0% ; Pred. No. 2.6e-28;				
Matches	92; Conservative 5; Mismatches 10; Indels 0; Gaps 0;				
Qy	129 DIELTOSPKFMSTSVDRTSVTCKASQVNQNTVKAQNSQSPKVLISASYRSGVPD 188				

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Scoring table:	BLOSUM62	ALIGNMENTS									
Gapopen:	10.0	PRT; 243 AA.									
Searched:	2166443 seqs, 705528306 residues	PRT; 243 AA.									
Total number of hits satisfying chosen parameters:	2166443	PRT; 243 AA.									
Minimum DB seq length:	0	PRT; 243 AA.									
Maximum DB seq length:	2000000000	PRT; 243 AA.									
Post-processing:	Minimum Match 0%	PRT; 243 AA.									
Database :	UniProt_05_80: 1: uniprot_sprot: 2: uniprot_trembl: *	PRT; 243 AA.									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.		PRT; 243 AA.									
SUMMARIES		PRT; 243 AA.									
Result No.	Score	Query	Match	Length	DB ID	Description					
1	783.5	56.2	243	2	Q7TQM2_MOUSE	Q7TQM2_MOUSE PRELIMINARY;	RESULT 1	Q7TQM2_MOUSE	PRT; 243 AA.		
2	725.5	52.0	255	2	Q6KB05_MOUSE	Q6KB05_MOUSE	Q7TQM2;	Q7TQM2;	PRT; 243 AA.		
3	724	51.9	244	2	Q65ZC8_HUMAN	Q65ZC8_homo sapien	DT 01-OCT-2003 (TREMBLrel. 25, Created)	DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)	PRT; 243 AA.		
4	708	50.8	487	2	Q65ZL2_HUMAN	Q65ZL2_mus sp. fv/	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)	PRT; 243 AA.		
5	669	48.0	240	2	Q65ZC9_HUMAN	Q65ZC9_homo sapien	DE SCFv 6H8 protein (Fragment).	DE SCFv 6H8 protein (Fragment).	PRT; 243 AA.		
6	630	45.2	241	2	Q921A6_MOUSE	Q921a6_mus musculu	GN Name=SCFv 6H8B;	GN Name=SCFv 6H8B;	PRT; 243 AA.		
7	584.5	41.9	248	2	Q65ZQ7_HUMAN	Q65ZQ7_mus sp. b3 (OS Mus musculus (Mouse).	OS Mus musculus (Mouse).	PRT; 243 AA.		
8	527	37.8	168	2	Q8VDC9_MOUSE	Q8VDC9_mus musculu	RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	PRT; 243 AA.		
9	520	37.3	468	2	Q66W9_MOUSE	Q66W9_mus musculu	NCBI TaxID=10050;	NCBI TaxID=10050;	PRT; 243 AA.		
10	516	37.0	121	1	HV01_MOUSE	HV01_mus musculu	RN [1]	RN [1]	PRT; 243 AA.		
11	515.5	37.0	218	2	Q925S1_MOUSE	Q925s1_mus musculu	RP NUCLEOTIDE SEQUENCE.	RP NUCLEOTIDE SEQUENCE.	PRT; 243 AA.		
12	514.5	36.9	613	2	Q8VCX7_MOUSE	Q8vcx7_mus musculu	RC STRAIN=Balb/C;	RC STRAIN=Balb/C;	PRT; 243 AA.		
13	494	35.4	108	2	Q8V1J0_MOUSE	Q8v1j0_mus musculu	RC MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;	RC MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;	PRT; 243 AA.		
14	491.5	35.2	143	2	Q91V67_MOUSE	Q91v67_mus musculu	RA Peter J.C.; Efeekhari P.; Billial P.; Wallukat G.; Hoebeke J.; RT "SCFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	RA Peter J.C.; Efeekhari P.; Billial P.; Wallukat G.; Hoebeke J.; RT "SCFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."	PRT; 243 AA.		
15	483	34.6	238	2	Q8PBV4_MOUSE	Q8pbv4_mus musculu	DR EMBL; AJ574851; CAB00495.1; -; Genomic_DNA.	DR EMBL; AJ574851; CAB00495.1; -; Genomic_DNA.	PRT; 243 AA.		
16	479	34.3	473	2	Q9PB84_MOUSE	Q9pb84_mus musculu	DR HSSP; P01751; 1A6W.	DR HSSP; P01751; 1A6W.	PRT; 243 AA.		
17	472	33.8	120	1	HV03_MOUSE	HV03_mus musculu	DR InterPro; IPR003596; Ig_v.	DR InterPro; IPR003596; Ig_v.	PRT; 243 AA.		
18	470.5	33.7	143	2	Q924Q0_MOUSE	Q924q0_mus musculu	DR SM00406; Ig_v.	DR SM00406; Ig_v.	PRT; 243 AA.		
19	467.5	33.5	145	2	Q924R3_MOUSE	Q924r3_mus musculu	DR PROSITE; PS50835; Ig_LIKE;	DR PROSITE; PS50835; Ig_LIKE;	PRT; 243 AA.		
20	464.5	33.3	463	2	Q99LC4_MOUSE	Q99lc4_mus musculu	FT NON_TER	FT NON_TER	PRT; 243 AA.		
21	464	33.3	117	1	HV12_MOUSE	HV12_mus musculu	SQ 3 QVQLQSGAELVRGTVKISCKASYYTFNWLGMVKQDQGHLEWIGDIYPGGGTYN 62	3 QVQLQSGAELVRGTVKISCKASYYTFNWLGMVKQDQGHLEWIGDIYPGGGTYN 62	PRT; 243 AA.		
22	464	33.3	144	2	Q924P5_MOUSE	Q924p5_mus musculu	Qy Query	Qy Query	PRT; 243 AA.		
23	464	33.3	458	2	Q8BJZ2_RAT	Q8bjz2_rat	Db Best Local Similarity 57.5%; Pred. No. 5.4%-56%; Mismatches 34; Conservative Matches 153; Gapsize 4;	Db Best Local Similarity 57.5%; Pred. No. 5.4%-56%; Mismatches 34; Conservative Matches 153; Gapsize 4;	PRT; 243 AA.		
24	463	33.2	117	1	HV13_MOUSE	HV13_mus musculu	Qy Query	Qy Query	PRT; 243 AA.		
25	462	33.1	149	1	KVSA_MOUSE	KVsa_mus musculu	Db 63 NEKFGRKATVTTADTSRTAYQVRSHTSEDAVYFCARSASWYFDWVGARTVTVSSAKT 12.2	Db 63 NEKFGRKATVTTADTSRTAYQVRSHTSEDAVYFCARSASWYFDWVGARTVTVSSAKT 12.2	PRT; 243 AA.		
26	462	33.1	486	2	QSHZY6_MOUSE	Qshzy6_mus musculu	Qy Query	Qy Query	PRT; 243 AA.		
27	460.5	33.0	481	2	Q91W71_MOUSE	Q91w71_mus musculu	Db 61 DEFKRK931LITVDTSSSTAMHLLSLASESDAVYYCARGRG-LDWGAGTLYTVSSGG 11.9	Db 61 DEFKRK931LITVDTSSSTAMHLLSLASESDAVYYCARGRG-LDWGAGTLYTVSSGG 11.9	PRT; 243 AA.		
28	459	32.9	483	2	Q5LUS1_MOUSE	Q5lus1_mus musculu	Qy Query	Qy Query	PRT; 243 AA.		
29	459	32.9	140	1	HV02_MOUSE	HV02_mus musculu	Db 180 SGMTSLSETGVSRFSGGSGKDYTLSTSLSQTDVATYYCQOYWS-TRTFGGGTKEIK- 23.7	Db 180 SGMTSLSETGVSRFSGGSGKDYTLSTSLSQTDVATYYCQOYWS-TRTFGGGTKEIK- 23.7	PRT; 243 AA.		
30	457	32.8	470	2	Q9TMK1_MOUSE	Q9tmk1_mus musculu	Qy Query	Qy Query	PRT; 243 AA.		
31	454.5	32.6	143	2	Q924P9_MOUSE	Q924p9_mus musculu			PRT; 243 AA.		

Qy	176 IYSASYRSGVPDRFTGSGSTDFTLTISNOSEDIAEYFCQQHTYPLTFGGTKLEIK	235	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
Db	181 HTIHYIOPIGIPSRFGSGSGRSYSSNLEPEDIATYCHYDNLH-TFEGGTKLEIK	239	DE Ant-MOG Z12 variable gamma 2a (Fragment).
Qy	236 RA 237		GN Name=IgG2a,
Db	240 RA 241		OS Mus musculus (Mouse).
			OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
			OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
			OC Muridae; Murinae; Mus.
			OX NCBI_TaxID=10090;
			RN [1]
			RP NUCLEOTIDE SEQUENCE.
			RC STRAIN=BALB/c;
			RA Sembi P.;
			RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
			RN [2]
			RP NUCLEOTIDE SEQUENCE.
			RC STRAIN=BALB/c;
			RA Cherniakovskiy Y.;
			RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
			DR AJ416332; CAC94867.1; - mRNA.
			DR HSSP; P01863; IBW.
			DR Q8VDC9; 20-168.
			DR Ensembl; ENSMUSG00000021155; Mus musculus.
			DR InterPro; IPR007110; Ig-like.
			DR InterPro; IPR03596; Ig-V.
			DR SMART; SM00406; IgV; 1.
			DR PROSITE; PSS0835; Ig_LIKE; 1.
			FT NON_TER 168 AA; 18293 MW; 1E3719FCOB7/2723 CRC64;
			SQ SEQUENCE 168 AA; 18293 MW;
Qy	Q5ZQ7_9MUR1 PRELIMINARY;	PRT; 248 AA.	Query Match 37.8%; Score 527; DB 2;
AC	Q5ZQ7_9MUR1		Best Local Similarity 78.2%; Pred. No. 3.5e-35;
DD	25-OCT-2004 (TREMBLrel. 28, Created)		Matches 97; Conservative 11; Mismatches 14; Indels 2; Gaps 1;
DR	25-OCT-2004 (TREMBLrel. 28, Last sequence update)		DR 2 AQQVQQSQGAELVPGTSVKISCKASGYFTINWLGWIKORGPHGEWIGDIYPGGYT 61
DR	25-OCT-2004 (TREMBLrel. 28, Last annotation update)		DR 19 SQVQLQSQSQAELMKPGASVVKISCKATGTYFESSYWIDWVKGKQRHGEWIGEILPGSRTN 78
DE	25 (Fv)-PE40 (Fragment).		DR 62 YNEKFKGKATVATDTSSRTAYVQRSLTSEDAVYFCAR--SASWYFDWGARTTVVSS 119
GN	Name=B3 (Fv)-PE40;		DR 79 YNEKFKGKTTFTADTSNTAYIQSSLTSEDAVYCANYGSSRWFDWGAGTCVVSS 138
OS	Mus sp.		SQ
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Query Match 41.9%; Score 584.5; DB 2;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		Best Local Similarity 47.8%; Pred. No. 1.e-39;
OC	Muridae; Murinae; Mus.		Matches 117; Conservative 42; Mismatches 73; Indels 13; Gaps 3;
OX			DR 139 TKT 142
			RESULT 9
Qy	4 VOLQQSGLAEVLVRPGTSVKISCKASGYFTINWLGWIKORGPHGEWIGDIYPGGYTNN 63		Q569W9_MOUSE PRELIMINARY; PRT; 468 AA.
Db	3 VKLVESGGSLVQPGESLKLSCATGFTSDYMMWWRTPKEKLEISNDSSAAYS 62		AC Q569W9;
Qy	64 EFKFGKATVATDTSSRTAYVQRSLTSEDAVYFCAR--SASWYFDWGARTTVVSSAK 121		DT 10-MAY-2005 (TREMBLrel. 30, Created)
Db	63 DTVKGKFTISRDNRANTLYQMSRLSKEDTAISCARGLAWGWEAVGQGTLYTVTSSGG 122		DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
Qy	122 TTPKLGG-----DIELTOSPKENMISTYGRDNVNTYKASQ----NYGTNVNAFWFOQKRGQ 170		DE Hypothetical protein.
Db	123 GGSGGGGGGGGGDVLMPLSPLSLDSAVFCARASW-YFDWGARTTVVSSAK 182		GN Name=Ig-1a;
Qy	171 SPKVLIYASRYSGVPDRFTGSGSTDFTLTISNOSEDIALYFCQQHTYPLTFEGGT 230		OS Mus musculus (Mouse).
Db	183 SPKVLIYKVSNRFSGPDRFSGSGTDETLKISRVEADLGYYCFQSHYBFTFGSGT 242		OC Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
Qy	231 KLEIK 235		OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Db	243 KLEIK 247		OC Muridae; Murinae; Mus.
			OX NCBI_TaxID=10090;
			RN [1]
			RP NUCLEOTIDE SEQUENCE.
			RC STRAIN=NCZEC II;
			RC TISSUE=tummary tumor metastasized to lung. Tumor arose spontaneously;
			RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.042603899;
			RA Strieber R.L.; Feingold E.A.; Grouse L.H.; Derge J.G.,
			RA Klausner R.D.; Collins F.S.; Wagner L.; Shenmen C.M.; Schuler G.D.,
			RA Altschul S.F.; Zeeberg B.; Buetow K.H.; Schaefer C.F., Bhat N.K.,
			RA Hopkins R.P.; Jordan H.; Moore T.; Max S.J.; Wang J., Hsieh F.,
			RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M., Hong L., Scheetz T.B.,
			RA Sharpleton M.; Sores M.B.; Donald M.F.; Casavant T.B., Prange C., Brownstein M.J.; Usdin T.B., Yoshiyuki S.; Carninci P., Mullany S.J., Raha S., Loqueilano N.A.; Peters G.J., Abramson R.D., Mullany S.J.,

RA	Bosak S.A., McEwan P.J.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalobos D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Heitton B., Ketteman N., Medan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalnus D.E., Schnerch A., Schein J.E., Jones J.S.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; RT
PR	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]	NUCLEOTIDE SEQUENCE.
RN	STRAN=CZBCH II;
RP	TISSUE=Mammary tumor metastatized to lung Tumor arose spontaneously;
RC	NIH MCC Project;
RG	Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
DR	EMBL; BC092271; AAH92271.1; -; mRNA.
DR	SMR; Q569W9; 20-464.
DR	MGI; MGI:96443; Igf-1a.
DR	GO; GO:0003823; F:antigen binding; IEA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR002710; Ig-like.
DR	InterPro; IPR003597; Ig_c1.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; cl-set; 3.
DR	SMART; SM00409; Ig; 2.
DR	SMART; SM00407; IgC1; 3.
DR	SMART; SM00406; IgV; 1.
DR	PROSITE; PS50835; Ig_LIKE; 4.
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SQ	SEQUENCE 468 AA; 51.666 MW; 5BF6E527329F8461 CRC64;
Qy	Query Match 37.3%; Score 50; DB 2; Length 468;
Db	Best Local Similarity 49.0%; Pred. No. 4.6e-34;
Matches	120; Conservative 31; Mismatches 54; Indels 40; Gaps
Qy	2 AYVOLQGSAELVRPGTTSVKSCKASGTYFTNTYWLGYKQRPGLENIGDLYPGGGTYN 6
Db	19 SEYVLOQGAEELVRPGSSVTKLSCXSGTFTS--VNWVQRPGLEWGHIPNGNTE 7
Qy	62 YNEKFKGAKATIQTDTSSRTAYIQVRSLSSEDSEAVYFCARSASW--YEDYWGARTTVYSS 11
Db	79 YNEKFKGATIQTDTSSRTAYIQVRSLSSENALYFCARTGGDGYFDWGOGTITVSS 11
Qy	120 AKTPKULQGSDIELTQSPEMSTVGDYRNVNTYKASONVETNV-AWFQQKPGQSPKVLIVS 1
Db	139 AKTT-----APSVTPLAPCGD---TTGSVTLGCLVKGYPFE----PVTLTWN 11
Qy	179 ASTRYS3V-----PDRFTGSGSGTDFLTINVOSEDLEYFCOOYHTPLFEGGGT 2
Db	181 SGGLSSGVTHTFPAPLQSDLYTSSS---VTVTSSTWPSOSIT--CNVRAHP----ASST 2
Qy	231 KLEIK 235
Db	230 KVDKK 234
RESULT 10	
HV01_MOUSE	
ID	HV01_MOUSE STANDARD
AC	P01745;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	10-MAY-2005 (Rel. 47, Last annotation update)
DE	Ig heavy chain V region MPC 11.
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Craniata; Chordata; Vertebrata; Buteleostomi; Muroidea; Muridae; Murinae; Muscarionotigures; Glirinae; Rodentia; Sciurognathi; OC

OX	NCBI_TaxID=10090;
RN	NUCLEOTIDE SEQUENCE
RN	MEDLINE=81053741;
RX	ZAKUT R., Cohen J.
RA	"Cloning and sequ-
RA	ing of immunoglobulin
RT	nucleic acids res-
RT	es.
RN	ERRATUM, AND SEQUE-
RN	Nucleic Acids Res
RN	CC -1- MISCELLANOUS
RN	CC -1- FROM A MYELOM
RN	CC -1- SIMILARITY: CC
CC	This Swiss-Prot entry
CC	between the Swiss-
CC	the European BioDB
CC	use as long as it is
CC	removed.
CC	PIR; A93708; GIWMS
DR	HSSP; P01751; INQI
DR	SMR; P01745; 1-12
DR	Ensembl; ENSMUSG01
DR	InterPro; IPR0071
DR	InterPro; IPR0035
DR	SMART; SM00406; IC
DR	PROSITE; PS05835; IC
KW	Immunoglobulin do-
FT	MAIN DOMAIN
FT	NON TER
FT	1
SQ	SEQUENCE 121 AA
Query Match	Best Local Similarity
Matches 94;	Conse
Qy	3 QVQLOQSG
Db	:
Db	1 EAQLOQSG
Qy	63 NEKFKGKA
Db	:
Db	61 NDNLKGKA
Qy	119 S 119
Db	121 S 121
RESULT 11	O92551_MOUSE
ID	O92551_MOUSE_PREL
AC	O92551;
DT	01-DEC-2001 (T-TERM)
DT	01-DEC-2001 (T-TERM)
DT	01-OCT-2003 (TRUNCATED)
DE	MRPS (Fragment).
OS	Mus musculus (Mouse)
OC	Mammalia; Eutheria;
OC	Muridae; Murinae;
OC	Caromyscinae;
OX	NCBI_TaxID=10090;
RN	NUCLEOTIDE SEQUE-
RN	STRAIN=BALB/C;
RN	PubMed=18196769;
RA	Cui D.X., Zeng G.
RA	Yan X.-J., Hou Y.-
RT	"Mechanism of exo-
RT	the repair of int-

RJL	World J. Gastroenterol. 6:709-717(2000).	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RN	[2]	RA	Schnecher A., Schein J.E., Jones S.J.M., Marra M.A., Marra M.A.;
	NUCLEOTIDE SEQUENCE.	RT	"Generation and initial analysis of more than 15,000 full-length human
RC	STRAIN:BALB/C;	RT	and mouse cDNA sequences";
RA	Cui D., Zeng G., Yan X., Li X., Su C.;	RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RJL	"Cloning of mouse genes related to repairing of intestinal epithelium	RL	[2]
RJL	of the irradiated mice by treatment with the intestinal RNA of mice of	RN	NUCLEOTIDE SEQUENCE.
RJL	the same strain.";	RC	STRAIN:FVB/N; TISSUE=Salivary gland;
RJL	Int. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).	RA	Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF240168; PAK43733.1; -; mRNA.	RJL	RJL [3]
DR	HSSP; P01665; 1QNZ.	RX	NUCLEOTIDE SEQUENCE.
DR	ENSEMBL; ENSEMBL00058040; Mus musculus.	PA	Sikder S.K., Borden P., Gruereo F., Akolkar P.N., Bhattacharya S.B.,
DR	InterPro; IPR007110; Ig-like.	RA	Morrison S.L., Kabat E.A.,
DR	SMART; SM00406; IgV; 1.	RT	"Amino acid substitutions in VH CDR2 change the idiotypic but not the antigen-binding of monoclonal antibodies to alpha(1---6) dextrans.";
DR	PROSITE; PS0835; Ig_LIKE; 1.	RT	J. Immunol. 142:188-193 (1989).
FT	NON_TER 218 218 AA;	RL	DR
FT	SEQUENCE 218 AA;	DR	ENMBL; BC018315; AAH18315.1; -; mRNA.
SC	527B4PA8F7982817 CRC64;	DR	PIR; C30562; C30562.
Query Match	37.0% ; Score 515.5 ; DB 2; Length 218;	DR	DR
Best Local Similarity	50.7% ; Prod. No. 4.2e-31; Gaps 5;	DR	HSSP; P01751; 1QEW.
Matches 110; Conservative	33; Mismatches 57; Indels 17; Gaps 5;	DR	Ensembl; ENSEMBL0000054328; Mus musculus.
Qy	1 MAQVQLQSGAELVYRPGTSVKISCKASGYTFINYWLGVKQRPKGHLWIGDIYPGGYT 60	DR	NCI; MGI: 96448; IgG-6.
Db	1 MAQVQLQSGAELVYRPGTSVKISCKASGYTFINYWLGVKQRPKGHLWIGDIYPGGYT 60	DR	GO; GO:0019815; C:B cell receptor complex; IDA.
Qy	61 NYNEKFKGKATVATDTSRATTAYQVRSLTSEDAVYFCARSASWYFD---YWGARTTVT 116	DR	GO; GO:0009897; C:external side of plasma membrane; IDA.
Db	61 KYAEKFGRGAFSLETSASTAYQISNLKEDATYFFMR---WDYDGFAYWGQTTVT 117	DR	GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
Qy	117 VSSAKTTPKLGG-----DIELTOSPKPMSTSVGDRVNVTYKASQ---NVGTN-VAWFOO 166	DR	GO; GO:0048711; C:perinuclear region, IDA.
Db	118 VSSGGCGGCGGGCGGGDIVLQSPLASLQGRATISCRASESYDNIGSEMFANWFOO 177	DR	GO; GO:0003823; P:antigen binding; IDA.
Qy	167 KPGGSPPKLIYASYYRSYKSCVDPRTGSSSGTDPFLTI 203	DR	GO; GO:0005515; P:protein binding; IPI.
Db	178 KPGGSPPKLIYASYYRSYKSCVDPRTGSSSGTDPFLTI 203	DR	GO; GO:0000187; P:transmembrane receptor activity; IDA.
Qy	Name=IgH-6;	DR	GO; GO:0003033; P:activation of MAPK activity; IDA.
Db	Mus musculus (Mouse).	DR	GO; GO:0005985; P:cell receptor signaling pathway; IDA.
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	DR	GO; GO:0045022; P:early endosome transport; IDA.
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	DR	GO; GO:0016064; P:humoral defense mechanism (sensu vertebralata); IDA.
OC	Muridae; Murinae; Mus.	DR	GO; GO:0030899; P:positive regulation of B cell proliferation; IDA.
OX	NCBI_TaxID=10090;	DR	GO; GO:0045807; P:positive regulation of endocytosis; IDA.
RN	[1]	DR	GO; GO:0005731; P:positive regulation of peptidyl-tyrosine phosphorylation; IDA.
RESULT 12	NUCLEOTIDE SEQUENCE.	DR	DR InterPro; IPR007110; Ig-like.
QBVCX7	QBVCX7 MOUSE PRELIMINARY;	DR	DR InterPro; IPR003597; Ig-cl.
ID	QBVCX7	DR	DR InterPro; IPR003006; Ig_MHC.
DT	01-MAR-2002 (TREMBLrel. 20, Created)	DR	DR InterPro; IPR003596; Ig_v.
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)	DR	SMART; SM00406; IgV; 1.
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)	DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_3.
DE	IgH-6 protein.	KW	Immunoglobulin domain.
GN	Name=IgH-6;	SEQUENCE	613 AA; 67855 MW; 41A9384DDA22862 CRC64;
Qy	36.9% ; Score 514.5 ; DB 2; Length 613;	Qy	2 AQVOLQSGAELVYRPGTSVKISCKASGYTFINYWLGVKQRPGHGLEWIGDIYPGGYTN 61
Db	Best Local Similarity 79.8%; Pred. No. 1.8e-33; Mismatches 12; Indels 1; Gaps 1;	Db	19 SQVOLQSGAELVYRPGAVKISCKATGYTFSSWVWYKQRPGHGLEWIGETLPGSSTN 78
Qy	95; Conservative 11; Mismatches 12; Indels 1; Gaps 1;	Qy	62 YNEKFKGKATVATDTSRATTAYQVRSLTSEDAVYFCARS-ASWYFDWYGARTTVTSS 119
Db	SEQUENCE 613 AA;	Db	79 YNEKFKGKATFADTSNTAYQVLSSLTSEDAVYFCARS-ASWYFDWYGARTTVTSS 137
Qy	RESULT 13	QBVJ0 MOUSE PRELIMINARY;	PRT; 108 AA.
Db	OBVJ0_MOUSE PRELIMINARY;	AC	OBVJ0_
Qy	OBVJ0_	DT	DT 01-MAR-2002 (TREMBLrel. 20, Created)
Db	OBVJ0_	DT	DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
Qy	OBVJ0_	DB	DB Anti-DNA light chain (Fragment).
Db	OBVJ0_	DT	DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
Qy	OBVJ0_	DB	DB Name=IgH-V19-14; Synonyms=V19-19;
Db	OBVJ0_	GN	GN Mus musculus (Mouse)
Qy	OBVJ0_	OS	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Db	OBVJ0_	OC	OC Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1] NUCLEOTIDE SEQUENCE.

RC STRAIN=C3H/HeJ-lpr/;

RX MEDLINE=96409289; PubMed=8814271;

RA Wloch M.K., Alexander A.M., Pisetty D.S., Gilkeson G.S.;

RT "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-lpr mice and lupus mice with nephritis.";

RR Eur. J. Immunol. 26:2225-2233(1996).

RN [2] NUCLEOTIDE SEQUENCE.

RX Pubmed=2499887;

RA Baccala R., Quang T.V., Gilbert M., Terrynck T., Avrameas S.;

RT "Two murine natural polyreactive autantibodies are encoded by nonmutated germ-line genes";

RR Proc. Natl. Acad. Sci. U.S.A. 86:4624-4628(1989).

RN [3] NUCLEOTIDE SEQUENCE.

RX MEDLINE=92381444; PubMed=1512540; DOI=10.1084/jem.176.3.761;

RA Tillman D.M., Jon N.T., Hill R.J., Marion T.N.;

RT "Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)F1 mice.";

RL J. Exp. Med. 176:761-779(1992).

RN [4] NUCLEOTIDE SEQUENCE.

RX MEDLINE=91115823; PubMed=1703527;

RA Goshorn S.C., Rezel E., Jeffereson R.;

RT "Common structural features among monoclonal antibodies binding the same antigenic region of cytochrome c.";

RL J. Biol. Chem. 266:2134-2142(1991).

DR EMBL; DR59155; AAB82917.1; -; mRNA..

DR PIR; A33933; A33933.

DR PIR; A37262; A37262.

DR PIR; PH1072; PH1072.

DR HSSP; P01634; 1IGC..

DR QBVLU0; 1-108.

DR Ensembl; ENSMUSG00000053690; Mus musculus.

DR MG1; MG1:1330830; Igk-V19-14.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003536; Ig_v..

DR SMART; SM00406; IgV; 1..

DR PROSITE; PS50835; Ig_LIKE; 1..

FT NON-TER 1 108 AA; 11859 MW; 68506D75613DBFB CRC64;

SEQ NUCLEOTIDE 108 AA; 11859 MW; 68506D75613DBFB CRC64;

Query Match Score 35.4%; Best Local Similarity 88.0%; Matches 95; Conservative 5; N mismatches 8; Indels 0; Gaps 0; Length 108;

QY 129 DIELTQSPEKMSSTSVGDYRNIVTYKASQNTVNAWFOOKPGQSPKVLYTASYRSGYPD 188

DB - 1 DWWQSTQFMSTSVGDYRVSTVKASQNTVNAWYQKPGQSPSKALYTASYRSPGYPFH 60

QY 189 RFTGSGSQTDTLITSNQSEDLAEEFCQOYHPLTFCGGTKLEIKR 236

DB - 61 RFTGSGSQTDTLITSNQSEDLAEEFCQOYNSTPYTFGGTKLEIKR 108

RESULT 14 Q91167_MOUSE PRELIMINARY; ID Q91167; PRT; 143 AA.

AC 091167_ MOUSE PRELIMINARY;

DT 01-DEC-2001 (TREMBrel. 19, Created)

DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)

DT 01-FEB-2005 (TREMBrel. 29, Last annotation update)

DT 01-FEB-2005 (TREMBrel. 29, Last protein (Fragment))

DR VH16-2-D-J-C mu protein (V304-D-J-C mu protein) (Fragment).

GN Name=VH16-2-D-J-C mu; Synonyms=V304-D-J-C mu;

OS Mus musculus (Mouse).

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FVB/N; TISSUE=Colon;
 RG NIH MGC Project ;
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC091754; AAH91754.1; -; mRNA.
 DR SMR; Q88EU4; 25-228.
 DR GO; GO:0003823; F-antigen binding; IBA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003577; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003396; Ig_v.
 DR Pfam; PF07654; C1-set; 1.
 DR SMART; SM00409; IgC; 2.
 DR SMART; SM00407; IgCl; 1.
 DR SMART; SM00406; IgV; 1.
 DR PROSITE; PS50835; Ig_LIKE; 2.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN 1.
 SEQUENCE 238 AA; AE2B2A90B9F7D5D CRC64;
 SQ

Query Match	34.6%	Score 493;	DB 2;	Length 238;
Best Local Similarity	82.3%	Pred. No. 2.1e-31;	Mismatches 9;	Indels 0;
Matches	93;	Conservative	11;	Gaps 0;

Qy 128 GDIBLTQSPKFMSTNSVGDRVNTYKASQNGITNAWFQOKPGSPKVLYIASASYRYGGVP 187
 Db 24 GDIWMTQSKPKFMSTSIGRVSITCKASQDVITAVWQOKPGSPKVLYIASASYRYGGVP 83

Qy 188 DRAFTGSGSGTDFLTISNVQSEDLAEYFCQQYHTYPLTFGGGTTKLEIKRADAA 240
 Db 84 DRAFTGSGSGTDFLTISNVQSEDADYFCQQYSSYPLTFGSGTKLEIKRADAA 136

Search completed: February 9, 2006, 03:33:22
 Job time : 165.118 secs

Qy 1 MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60
 Db 1 MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

Qy 61 NYNEKFKRATVADTSRPTAYQVRSLTSEDAVYFCARSASWYFDWGAFTTVVSA 120
 Db 61 NYSETFKRATLTVDTSSNTVMQLSSLTSEDAVYFCARGVG--LDWQGQTIVTVTSG 118

Qy 121 KTPKLGG----DIELTQSPKEMSTSAGDRVNTVYKASQNYGTNVAWFQOKPGSPKV 174
 Db 119 GCGGGGGGGGGSDIELTQSPKEMSTSIGDRITCASAQDVTAVGWIQRPQSPKL 178

Qy 175 LIYSASYRSVGVPDRFTSGSGDFTLTISNOSEDLAYFCQYHPPPLTFFGGTKBKI 234
 Db 179 LIFWSSTRHTGVPDFRTSGSGDFTLTISNOSEDLDYFCHQYSSYPTFGSGTKBKI 238

Qy 235 KR 236
 Db 239 KR 240

RESULT 7
 US-10-092-246-35
 ; Sequence 35, Application US/10092246
 ; Patent No. 6501314

; GENERAL INFORMATION;
; APPLICANT: The Minister of National Defence, Government of Canada
; APPLICANT: Fulton, R E
; APPLICANT: Alvi, Azhar E
; APPLICANT: Nagata, Leslie
; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Monoclonal Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
; FILE REFERENCE: NEI-0007
; CURRENT APPLICATION NUMBER: US/10/092-246
; CURRENT FILING DATE: 2002-03-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 35
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
 US-10-092-246-35

Query Match 61.1%; Score 853; DB 2; Length 240;
 Best Local Similarity 68.6%; Pred. No. 6.e-62; Mismatches 43; Indels 8; Gaps 2;
 Matches 166; Conservative 166; Mismatches 24; Indels 44; Gaps 8;

Qy 1 MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60
 Db 1 MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

Qy 61 NYNEKFKRATVADTSRPTAYQVRSLTSEDAVYFCARSASWYFDWGAFTTVVSA 120
 Db 61 NYSETFKRATLTVDTSSNTVMQLSSLTSEDAVYFCARGVG--LDWQGQTIVTVTSG 118

Qy 121 KTPKLGG----DIELTQSPKEMSTSAGDRVNTVYKASQNYGTNVAWFQOKPGSPKV 174
 Db 119 GCGGGGGGGGGSDIELTQSPKEMSTSIGDRITCASAQDVTAVGWIQRPQSPKL 178

Qy 175 LIYSASYRSVGVPDRFTSGSGDFTLTISNOSEDLAYFCQYHPPPLTFFGGTKBKI 234
 Db 179 LIFWSSTRHTGVPDFRTSGSGDFTLTISNOSEDLDYFCHQYSSYPTFGSGTKBKI 238

Qy 235 KR 236
 Db 239 KR 240

RESULT 9

US-10-092-246-37

; Sequence 37, Application US/10092246

; Patent No. 6501314

; GENERAL INFORMATION;

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R E

; APPLICANT: Alvi, Azhar E

; APPLICANT: Nagata, Leslie

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Monoclonal Antibody Against Venezuelan Equine Encephalitis Virus (Vee)

; FILE REFERENCE: NEI-0007

; CURRENT APPLICATION NUMBER: US/10/092-246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 37

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A4A1

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/092-246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

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; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

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; NUMBER OF SEQ ID NOS: 39

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; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

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; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

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; SOFTWARE: PatentIn version 3.2

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; TYPE: PRT

; ORGANISM: mouse

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; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

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; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

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; TYPE: PRT

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; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

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; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

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; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

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; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

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; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

; DB: MAQVLOQSGPVELVKPGASKVSKCKASGYTFYHVVKGPKGQGLEWIGIYTGPFDNT 60

; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

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; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: mouse

; QUERY: MAQVLOQSGAELVRPGTSVKISCKASSGYTFNYWLGVKQRPCHGLEWIGDIYPGGYT 60

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; CURRENT APPLICATION NUMBER: US/10/096-246A

; CURRENT FILING DATE: 2002-03-13

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; SOFTWARE: PatentIn version 3.2

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; LENGTH: 240

; TYPE: P

Qy 61 NYNEKPKGKATVADTSRTAYQVRSLTSEDSAVYFCARSASWYFPDWGARTTVYSSA 120
 Db 61 NYSETFKGKATVADTSRTAYQVRSLTSEDSAVYFCARGVG-LDYGQGTIVTYSQ 118
 Qy 121 KTPKLGG-----DIELTQSPKEMTSVGRDNVTVYKASQNVGTINAVFOOKPQSPKV 174
 Db 119 GGGGGGGGGGGSDELITQSPNLSLSTSGDRIRITCKASQDVDTAVGYQRPQSPKL 178
 Qy 175 LIYASRYSGVPDRFTGSSTDFTLTISNVQSEDLEYFCQOYHTPLTFGGTKEI 234
 Db 179 LIFWSSTRHTGVPDFRTGSSTDFTLTISNVQSEDLEYFCHQYSSSPFTFGSGTKEI 238
 Qy 235 KR 236
 Db 239 KR 240

RESULT 10
 US-10-092-246-33
 ; Sequence 33, Application US/10092246
 ; Patent No. 6501314
 ; GENERAL INFORMATION:
 ; APPLICANT: Fulton, R E
 ; ALVI, Azhar E
 ; APPLICANT: Nagata, Leslie
 ; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc
 ; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)
 ; FILE REFERENCE: NEL-0007
 ; CURRENT APPLICATION NUMBER: US/10/092,246
 ; CURRENT FILING DATE: 2002-03-13
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 33
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Mouse hybridoma cell line 1A1A1
 ; US-10-092-246-33

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Qy 61 NYNEKPKGKATVADTSRTAYQVRSLTSEDSAVYFCARSASWYFPDWGARTTVYSSA 120
 Db 61 NYSETFKGKATVADTSRTAYQVRSLTSEDSAVYFCARGVG-LDYGQGTIVTYSQ 118
 Qy 121 KTPKLGG-----DIELTQSPKEMTSVGRDNVTVYKASQNVGTINAVFOOKPQSPKV 174
 Db 119 GGGGGGGGGGGSDELITQSPNLSLSTSGDRIRITCKASQDVDTAVGYQRPQSPKL 178
 Qy 175 LIYASRYSGVPDRFTGSSTDFTLTISNVQSEDLEYFCQOYHTPLTFGGTKEI 234
 Db 179 LIFWSSTRHTGVPDFRTGSSTDFTLTISNVQSEDLEYFCHQYSSSPFTFGSGTKEI 238
 Qy 235 KR 236
 Db 239 KR 239

; TITLE OF INVENTION: Monoclonal ScFv Antibody Against Venezuelan Equine Encephalitis

; TITLE OF INVENTION: Virus (Vee)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/096,246A

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO: 33

; LENGTH: 239

; TYPE: PRT

; ORGANISM: mouse

; US-10-096-246A-33

Query Match 58.7%; Score 819.5; DB 2; Length 239;

Best Local Similarity 67.4%; Pred. No. 3.7e-59;
 Matches 163; Conservative 24; Mismatches 46; Indels 9; Gaps 3;

Qy 1 MAQVOLQOSGABLVPGTSVYKISCKASGYFTNTWLGWYKPGHGLEWIGDIYPGGYT 60
 Db 1 MAQVOLQESGPVELVKPGASTVYKISCKASGYFTNTWLGWYKPGHGLEWIGDIYPGGYT 60

Qy 61 NYNEKPKGKATVADTSRTAYQVRSLTSEDSAVYFCARSASWYFPDWGARTTVYSSA 120
 Db 61 NYSETFKGKATVADTSRTAYQVRSLTSEDSAVYFCARGVG-LDYGQGTIVTYSQ 118

Qy 121 KTPKLGG-----DIELTQSPKEMTSVGRDNVTVYKASQNVGTINAVFOOKPQSPKV 174
 Db 119 GGGGGGGGGGGSDSSLLVS-KFVTSIGDRIRITCKASQDVDTAVGYQRPQSPKL 177

Qy 175 LIYASRYSGVPDRFTGSSTDFTLTISNVQSEDLEYFCQOYHTPLTFGGTKEI 234
 Db 178 LIFWSSTRHTGVPDFRTGSSTDFTLTISNVQSEDLEYFCHQYSSPFEGSGTKEI 237

Qy 235 KR 236

Db 238 KR 239

RESULT 12

US-10-092-246-2

; Sequence 2, Application US/10092246

; Patent No. 6501314

; GENERAL INFORMATION:

; APPLICANT: The Minister of National Defence, Government of Canada

; APPLICANT: Fulton, R E

; APPLICANT: Nagata, Leslie

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc

; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis Virus (Vee)

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10/092,246

; CURRENT FILING DATE: 2002-03-13

; NUMBER OF SEQ ID NOS: 37

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO: 2

; LENGTH: 257

; TYPE: PRT

; ORGANISM: Mouse hybridoma cell line 1A1A1

; US-10-092-246-2

Query Match 58.4%; Score 814.5; DB 2; Length 257;

Best Local Similarity 66.0%; Pred. No. 1e-58;
 Matches 163; Conservative 25; Mismatches 50; Indels 9; Gaps 3;

Qy 1 MAQVOLQOSGABLVPGTSVYKISCKASGYFTNTWLGWYKPGHGLEWIGDIYPGGYT 60
 Db 1 MAQVOLQESGPVELVKPGASTVYKISCKASGYFTNTWLGWYKPGHGLEWIGDIYPGGYT 60

Qy 61 NYNEKPKGKATVADTSRTAYQVRSLTSEDSAVYFCARSASWYFPDWGARTTVYSSA 120
 Db 61 NYSETFKGKATVADTSRTAYQVRSLTSEDSAVYFCARGVG-LDYGQGTIVTYSQ 118

Qy 121 KTPKLGG-----DIELTQSPKEMTSVGRDNVTVYKASQNVGTINAVFOOKPQSPKV 174
 Db 119 GGGGGGGGGGGSDSSLLVS-KFVTSIGDRIRITCKASQDVDTAVGYQRPQSPKL 177

Qy 175 LIYASRYSGVPDRFTGSSTDFTLTISNVQSEDLEYFCQOYHTPLTFGGTKEI 234
 Db 178 LIFWSSTRHTGVPDFRTGSSTDFTLTISNVQSEDLEYFCHQYSSPFEGSGTKEI 237

Qy 235 KR 236

Db 238 KR 239

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc

; TITLE OF INVENTION: scFv Antibody Against Venezuelan Equine Encephalitis

; FILE REFERENCE: NEL-0007

; CURRENT APPLICATION NUMBER: US/10096246A

; Patent No. 6818748

; GENERAL INFORMATION:

; APPLICANT: Fulton, R. Elaine

; APPLICANT: Nagata, Leslie

; APPLICANT: Alvi, Azhar Z.

; TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of Mc

Qy	63	NEKFKGKATVADTSRATVQVQVRSLTSEDSAVYFCARSASWYFDWVGARTTVSSAKT	122
Db	61	NQKPSKATITVDKSSSTMEHSUTSSESAVYCARSS--PDWQGCTTVSSG-	116
Qy	123	TPKLGGS-----DIELTOSPKENSTSVDRLNVTYKASQNVGTINANFQQKPEQ	170
Db	117	----GGGGGGYVGSGGGSD.QMTQSPSSLSASLGEDTTITCHASQINWLSWYQKPCN	172
Qy	171	SPKVLIYASASYRYSGYVPDRFTGSGSGTDFLTISVQSEDLAECQOYHTYPLTEGGST	230
Db	173	IPKLIYRASNLTGVPSSRGSGSGTGFLLTISSLQPBDIATTYCQOQSYPLTEGGST	232
Qy	231	KLEIKRADA---AAAGSERKLISEDLN	255
Db	233	KLEIKRABAAPHHHHNGAERKLISEDLN	261

Search completed: February 9, 2006, 03:35:34
Job time : 35.7701 secs

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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: February 9, 2006, 03:53:23 ; Search time 122.43 Seconds

894.155 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQYOLQQSGAABLVRPGTSV.....GSEQLISBEDLNHHHHH 262

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Maximum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
 1: /cgns2_6_ptodata/1/pubpa/us07_pubcomb.pep:
 2: /cgns2_6_ptodata/1/pubpa/us08_pubcomb.pep:
 3: /cgns2_6_ptodata/1/pubpa/us09_pubcomb.pep:
 4: /cgns2_6_ptodata/1/pubpa/us10_pubcomb.pep:
 5: /cgns2_6_ptodata/1/pubpa/us10b_pubcomb.pep:
 6: /cgns2_6_ptodata/1/pubpa/us11_pubcomb.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	899.5	64.2	240	5	US-10-482-630-51	Sequence 51, Appl
2	891.5	63.9	296	5	US-10-784-105-2	Sequence 2, Appl
3	862.5	61.8	249	3	US-09-984-186-18	Sequence 18, Appl
4	862.5	61.8	249	4	US-10-237-667-18	Sequence 18, Appl
5	862.5	61.8	249	4	US-10-237-708-18	Sequence 18, Appl
6	862.5	61.8	249	4	US-10-237-866-18	Sequence 18, Appl
7	862.5	61.8	249	4	US-10-237-871-18	Sequence 18, Appl
8	862.5	61.8	249	4	US-10-237-924-18	Sequence 18, Appl
9	862.5	61.8	249	4	US-10-702-536-18	Sequence 18, Appl
10	862.5	61.8	249	5	US-10-702-536-18	Sequence 18, Appl
11	862.5	61.8	249	6	US-11-146-077-18	Sequence 18, Appl
12	862.5	61.8	622	4	US-10-378-832A-2	Sequence 2, Appl
13	856.5	61.4	255	5	US-10-511-94-21	Sequence 21, Appl
14	856	61.4	240	4	US-10-096-246-36	Sequence 36, Appl
15	853	61.1	240	4	US-10-096-246-35	Sequence 35, Appl
16	847.5	60.8	243	5	US-10-879-994-10	Sequence 10, Appl
17	847.5	60.8	243	5	US-10-610-452-10	Sequence 10, Appl
18	846	60.6	258	4	US-10-239-656-59	Sequence 59, Appl
19	842.5	60.4	291	6	US-11-093-103-102	Sequence 102, Appl
20	841	60.3	240	4	US-10-096-246-37	Sequence 37, Appl
21	829.5	59.5	331	4	US-10-059-261-169	Sequence 169, Appl
22	829.5	59.5	331	5	US-10-059-649-169	Sequence 33, Appl
23	819.5	58.7	239	4	US-10-059-646-33	Sequence 2, Appl
24	814.5	58.4	257	4	US-10-096-246-2	Sequence 2, Appl
25	811	58.1	264	4	US-10-114-716A-46	Sequence 46, Appl
26	811	58.1	264	5	US-10-930-548-46	Sequence 46, Appl
27	808	57.9	240	4	US-10-096-246-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-10-482-630-51
; Sequence 51, Application US/10482630
; Publication No. US20040244851A1

; GENERAL INFORMATION:
 ; APPLICANT: Zhu, Zhenping
 ; TITLE OF INVENTION: Bispecific Antibodies That Bind to VEGF Receptors
 ; FILE REFERENCE: 11245/4802
 ; CURRENT APPLICATION NUMBER: US/10/482,630
 ; CURRENT FILING DATE: 2003-12-23
 ; PRIORITY APPLICATION NUMBER: PCT/US02/20332
 ; PRIORITY FILING DATE: 2002-06-26
 ; PRIORITY APPLICATION NUMBER: US 6/301,299
 ; PRIORITY FILING DATE: 2001-06-26
 ; NUMBER OF SEQ ID NOS: 137
 ; SOFTWARE: WordPerfect 8.0 for Windows
 ; SEQ ID NO: 51
 ; LENGTH: 240
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ;
 US-10-482-630-51

Query Match Score 895.5; DB 5; Length 240;
 Best Local Similarity 64.2%; Pred. No. 3; Mismatches 20; Indels 7; Gaps 2;
 Matches 178; Conservative 20;

QY	3	QVQLQSGAELVPRGTTSVKLSCKASGKQTPNNMGLWKRQGPGRHLIEWIGDIPGGGTYN
Db	1	QVKLQSGAELVPRGTTSVKLSCKASGFKNDTYYTHWKQSPPEQGLWIGMDPPNDNTKV
QY	63	NEKFKGKATVTDSSRTAVQVSLSLSDSAVFCARSASWYDVGARTTVTSSAKT 122
Db	61	DPKFQKATITADSSNTAYMQLSLSTSDDTAVYCA-LPPFYFDWGHGTTVSSGGG 119
QY	123	TPKLG-----DELTQSFKFMSTSVGDRVVNTYKASQNGTYAWFOQRPQGSQPKVLI 176
Db	120	GSGGGGGGGGGSDLTQSPKFMSTSVGDRVSVTCASQNDTIVAWYQKPGQSPKALI 179
QY	177	YSASTRYSGYPDRFGSGSGTDFLTUTISVQSEDAEYPCQOQHMYPLTFGGGTVKLBIKR 236
Db	180	YSASTRYSGVPDRFGSGSGTDFLTUTISVQSEDAEYFCQOQHMYPLTFGGGTVKLBIKR 239

RESULT 2
US-10-784-305-2
; Sequence 2, Application US/10784305
;

Publication No. US20050118569A1
 GENERAL INFORMATION:
 APPLICANT: Fulton, R. Elaine
 APPLICANT: Nagata, Leslie P.
 APPLICANT: Alvi, Azhar Z.
 APPLICANT: Hu, Wei-Gang
 TITLE OF INVENTION: Genetic Engineering of Streptavidin-Binding Peptide Tagged Single-Chain Variable Fragment Antibody to Venezuelan Equine Encephalitis Virus

CURRENT APPLICATION NUMBER: US/10/784,305
 CURRENT FILING DATE: 2004-02-24
 PRIOR APPLICATION NUMBER: 60/448,902
 PRIOR FILING DATE: 2003-02-24
 NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 2
 LENGTH: 296
 TYPE: PRT
 ORGANISM: Mouse
 FEATURE:
 NAME/KEY: MISC FEATURE
 OTHER INFORMATION: scFv, 1-269;
 OTHER INFORMATION: SBP, 6His and spaces: 270-296
 US-10-784-305-2

Query Match 63.9%; Score 801.5; DB 5; Length 296;
 Best Local Similarity 64.8%; Pred. No. 8.7e-60;
 Matches 177; Conservative 26; Mismatches 57; Indels 13; Gaps 3;

Db 26 MAQVQLQSGAELVRPGTSVKISCKASGYTFTNYWLGTVKORPGHGLEWIGDLYPGCGYT 60
 Db 26 MAQVQLQSGAELVRPGTSVKISCKASGYTFTNYWLGTVKORPGHGLEWIGDLYPGCGYT 85

Qy 1 MAQVQLQSGAELVRPGTSVKISCKASGYTFTNYWLGTVKORPGHGLEWIGDLYPGCGYT 60
 Db 121 KTPKLGG-----DIETLQSPRMSTGDRNTVYQVSLSITSEDAVYFCARSASWYEDWVGA
 Qy 61 NYNEKEFKSKATVADTSRTAYVQVSLSITSEDAVYFCARSASWYEDWVGA
 Db 86 NYSETFKGRATVYDTSENIVMQLSSTSIGDRIRTCASODVYFCARGVGS-LDVWGOQTIVTWSG 143

Qy 175 LIYSASYRSGVPDRFTSGSGTDFLTISINVQSEDILAYFCQOYHTPLTRFGGTKEI 234
 Db 204 LIFPSSTRHTGVDPFRFTSGSGTDFLTISINVQSEDILADYFCHQYSSPPTFQSGTKEI 263

Qy 235 KRADAANGS----EQKLISEEDLNSHHHHH 262
 Db 264 KRAAAHSGGGCPHPFRYAGGGSHHHHH 296

RESULT 3
 US-09-984-186-18
 Sequence 18, Application US/09984186
 Patent No. US20020151011A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guittot, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSES: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/984,186
 FILING DATE: 29-Oct-2001
 CLASSIFICATION: -Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US 08/256,927
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph.D., Julie K.
 REGISTRATION NUMBER: P-38 619
 REFERENCE/DOCKET NUMBER: S192006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-1839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 18:
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-984-186-18

Query Match 61.8%; Score 862.5; DB 3; Length 249;
 Best Local Similarity 69.5%; Pred. No. 1.2e-57;
 Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

Qy 3 OYLOQSGAELVRPGTSVKISCKASGYTFTNYWLGTVKORPGHGLEWIGDLYPGCGYT 62
 Db 4 QYOLEQSPELYVRPGTSVKISCKASGYTFTNYWLGTVKORPGHGLEWIGDLYPGCGYT 63

Qy 63 NEKFKGKATVADTSRTAYVQVSLSITSEDAVYFCARSAS-----WYFDWGMARTV 115
 Db 64 NGRFKGKATVADTSRTAYMQLSLTSIVSGAVYFCAKENNRFDERGYAMDYWGQTTV 123

Qy 116 TVSSAKTTPKLGG-----DIBETQSPRMSTGDRNTVYQVSLSITSEDAVYFCARSAS 169
 Db 124 TVSSGGGGGGGGGGGGGGNNIQLTQSPNSMTSGDRVSTICKASQDVDTSVAWQQKPG 183

Qy 170 QSPKVLISASRYSGVPDRFTSGSGTDFLTISINVQSEDILAEYFCQOYHTPLTRFGGG 229
 Db 184 QSPKVLISASRYSGVPDRFTSGSGTDFLTISINVQSEDILAEYFCQOYHTPLTRFGGG 243

RESULT 4
 US-10-237-667-18
 Sequence 18, Application US/10237667
 Publication No. US200300223081
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guittot, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, COMPOSITION PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA

ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,667
FILING DATE: 10-SEP-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01054
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 249 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-667-18

Query Match 61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-57;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

US-10-237-708-18

Qy	3	QVQLQSGAIGAIIVRPGTGSVKISCKSKASCGYTFITNYLGHWKQRPGHGIEWIGDLYPGGGTYN	62	Query Match 61.8%; Score 862.5; DB 4; Length 249;	
Db	4	QVQLEQSGPVELVKPGASKVLSKCKSKASCGYAFRSWMMWVKQRPQGQGLWIGIYPGDTRV	63	Best Local Similarity 69.5%; Pred. No. 1.2e-57;	
Qy	63	NBKPKGKATVADTSRRTAVQVRSLTSEDAVYFCRSAS-----WYFDWNGARTY	115	Mismatches 40; Indels 13; Gaps 2;	
Db	64	NGKFKGKATVADTSRRTAVQVRSLTSEDAVYFCRSAS-----WYFDWNGARTY	123	SEQUENCE DESCRIPTION: SEQ ID NO: 18:	
Qy	116	TVSSAKTTPKLG-----DIBLTQSPKEMSTSVDGRVNVTYKAQNQVGTVNVAWQQKPG	169	3 QVQLQSGAIGAIIVRPGTGSVKISCKSKASCGYTFITNYLGHWKQRPGHGIEWIGDLYPGGGTYN	62
Db	124	TVSSGGGGGGGGGGSNQLTQSPMSSTSVDGRVNVTICKAQDVTISVAWQQKPG	183	4 QVQLEQSGPVELVKPGASKVLSKCKSKASCGYAFRSWMMWVKQRPQGQGLWIGIYPGDTRV	63
Qy	170	QSPKLUYLASYRYSCUPDRFTGSQGSDTFLTISVQSELAEYFCQQTHTYPLTEGGG	229	63 NBKPKGKATVADTSRRTAVQVRSLTSEDAVYFCRSAS-----WYFDWNGARTY	115
Db	184	QSPKLUYLASYRYSCUPDRFTGSQGSDTFLTISVQSEDAVYFCQQTHTYPLTEGGG	243	64 NGKFKGKATVADTSRRTAVQVRSLTSEDAVYFCRSAS-----WYFDWNGARTY	123
Qy	230	TKLEIK 235		116 TVSSAKTTPKLG-----DIBLTQSPKEMSTSVDGRVNVTYKAQNQVGTVNVAWQQKPG	169
Db	244	TKLEIK 249		124 TVSSGGGGGGGGGGSNQLTQSPMSSTSVDGRVNVTICKAQDVTISVAWQQKPG	183
Qy	230	TKLEIK 235		170 QSPKLUYLASYRYSCUPDRFTGSQGSDTFLTISVQSEDAVYFCRSAS-----WYFDWNGARTY	115
Db	244	TKLEIK 249		170 QSPKLUYLASYRYSCUPDRFTGSQGSDTFLTISVQSEDAVYFCRSAS-----WYFDWNGARTY	123
Qy	230	TKLEIK 235		184 QSPKLUYLASYRYSCUPDRFTGSQGSDTFLTISVQSEDAVYFCRSAS-----WYFDWNGARTY	169
Db	244	TKLEIK 249		184 QSPKLUYLASYRYSCUPDRFTGSQGSDTFLTISVQSEDAVYFCRSAS-----WYFDWNGARTY	183

RESULT 5
US-10-237-708-18
Sequence 18, Application US/10237708
Publication No. US200303610A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guitton, Jean-Dominique

US-10-237-866-18
 ; Sequence 18; Application US/10237866
 ; Publication No. US20030036171A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Pournier, Alain
 Guittot, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice

Jung, Gerard
 Yeh, Patrice

RESULT 7
 US-10-237-871-18
 ; Sequence 18; Application US/10237871
 ; Publication No. US20030036172A1
 GENERAL INFORMATION:
 APPLICANT: Fleer, Reinhard
 Fournier, Alain
 Guittot, Jean-Dominique
 Jung, Gerard
 Yeh, Patrice

TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
 PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
 CONTAINING SAID POLYPEPTIDES

NUMBER OF SEQUENCES : 36

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,866
 FILING DATE: 10-Sep-2002
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 28-JAN-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST20006-US

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808

INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 249 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:

US-10-237-866-18

Query Match 61.8%; Score 862.5; DB 4; Length 249;
 Best Local Similarity 69.5%; Pred. No. 1.2e-57;
 Matches 171; Conservative 22; MisMatches 40; Indels 13; Gaps 2;

3 QVQLQGSQAAELVRGTSYKISCKASGYFTFTNYLGWYKQRPGLGLEWIGDIYPGGGTNY 62
 4 QVQLEQSGPBLVKRGASVKISCKASGYAFSRSMMWYKQPGGLEWIGRIYPGDGDKY 63

63 NEKPKGKATVYADTSSRATAYVQYRSLSEDSAVYFCARSAS-----WYFDWGWARTV 115
 64 NGKPKGKATVYADRSSATAYMQLSSLTVGSAVYFCAEENNRFDERGYAMDYWGQGRTV 123

116 TVSSAKTRPKLGG----DIELTOSPKFMSYGVDRNVTYKASQNGTNYAWFOQPG 169
 124 TVSSGGGGCGGGCGGGCGNIOLQSPMSMTSYGVDRSITCAQDQDTSWAVYQKPG 183

Qy 3 QVQLQGSQAAELVRGTSYKISCKASGYFTFTNYLGWYKQRPGLGLEWIGDIYPGGGTNY 62
 Db 4 QVQLEQSGPBLVKRGASVKISCKASGYAFSRSMMWYKQPGGLEWIGRIYPGDGDKY 63

Qy 3 NEKPKGKATVYADTSSRATAYVQYRSLSEDSAVYFCARSAS-----WYFDWGWARTV 115
 Db 4 NGKPKGKATVYADRSSATAYMQLSSLTVGSAVYFCAEENNRFDERGYAMDYWGQGRTV 123

Qy 170 QSPKVLYIASRYVSGPDRFTGGSGDFTLTTISNOYSEDLABYFCQQHHTYPLTFCGG 229
 Db 184 QSPKLILITWAISTRHTGVPDFRTGGSGDFTLTTISNOYSEDLABYFCQQSSYWPWFCGG 243

Qy 230 TKLEIK 235
 Db 244 TKLEIK 249

Qy 230 TKLEIK 235
 Db 244 TKLEIK 249

NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Rhone-Poulenc Rorer Inc.
 STREET: 500 Arcola Road, 3C43
 CITY: Collegeville
 STATE: PA
 COUNTRY: USA
 ZIP: 19426
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: Macintosh
 OPERATING SYSTEM: System 7.1
 SOFTWARE: Word 5.1 (PatentIn)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/237,871
 FILING DATE: 10-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/FR93/00085
 FILING DATE: 31-JAN-1997
 APPLICATION NUMBER: US/08/797,689
 FILING DATE: 28-JUL-1994
 APPLICATION NUMBER: FR 92/01064
 FILING DATE: 31-JAN-1992
 APPLICATION NUMBER: PCT/FR93/00085
 ATTORNEY/AGENT INFORMATION:
 NAME: Smith Ph.D., Julie K.
 REGISTRATION NUMBER: P-38,619
 REFERENCE/DOCKET NUMBER: ST20006-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (610) 454-3839
 TELEFAX: (610) 454-3808
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 249 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-10-237-866-18

US-10-237-871-18

Query Match 61.8%; Score 862.5; DB 4; Length 249;
 Best Local Similarity 69.5%; Pred. No. 1.2e-57;
 Matches 171; Conservative 22; MisMatches 40; Indels 13; Gaps 2;

3 QVQLQGSQAAELVRGTSYKISCKASGYFTFTNYLGWYKQRPGLGLEWIGDIYPGGGTNY 62
 4 QVQLEQSGPBLVKRGASVKISCKASGYAFSRSMMWYKQPGGLEWIGRIYPGDGDKY 63

63 NEKPKGKATVYADTSSRATAYVQYRSLSEDSAVYFCARSAS-----WYFDWGWARTV 115
 64 NGKPKGKATVYADRSSATAYMQLSSLTVGSAVYFCAEENNRFDERGYAMDYWGQGRTV 123

116 TVSSAKTRPKLGG----DIELTOSPKFMSYGVDRNVTYKASQNGTNYAWFOQPG 169
 124 TVSSGGGGCGGGCGGGCGNIOLQSPMSMTSYGVDRSITCAQDQDTSWAVYQKPG 183

Qy 3 NEKPKGKATVYADTSSRATAYVQYRSLSEDSAVYFCARSAS-----WYFDWGWARTV 115
 Db 4 NGKPKGKATVYADRSSATAYMQLSSLTVGSAVYFCAEENNRFDERGYAMDYWGQGRTV 123

RESULT 8
US-10-237-624-18
Sequence 18, Application US/10237624
Publication No. US2003008274A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guittot, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/237,624
FILING DATE: 10-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
LENGTH: 249 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-237-624-18

Query Match 61.8%; Score 862.5; DB 4; Length 249;
Best Local Similarity 69.5%; Pred. No. 1.2e-7;
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;

3 QVQLOQSGAELVRPGT3VKISCKASGYTFTNYWLGNVKORDPHGLEWIGD1YPGG3YTNY 62

QY 116 TVSSAKTPKLGG-----DIELTQSPKPMSTSVDRLVNTYKASQNTGTVNWAFOQPG 169
Db 124 TVSSGGGSGCCGCGGCCNNIQLQTSPMSMSTSVDRLVNTYKASQNTGTVNWAFOQPG 183
QY 170 QSPKVLIYSASYRSYGVPDFGTGGSGTDFLTATISNVOSEDLEYFCQQHTYPLTFCGG 229
Db 184 QSPKLITIWASTRHTGVPDFGTGGSGTDFLTATISNVOSEDADYFCQQSSXPWTFCGG 243
QY 230 TKLEIK 235
Db 244 TKLEIK 249

RESULT 9
US-10-702-536-18
Sequence 18, Application US/10702536
Publication No. US20040088976A1
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Fournier, Alain
Guittot, Jean-Dominique
Jung, Gerard
Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES, PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (PatentIn)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/702,536
FILING DATE: 07-Nov-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US/08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3839
TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
LENGTH: 249 amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:

4 QVQLEQSGPVELVKPGASVKISCKASGYTFTNYWLGNVKORDPHGLEWIGD1YPGG3YTNY 63
63 NERPKGRKATVTDSSRTAYVQVRSRSLTSBDSAVYFCARSAS-----WYFDWGRARTYV 115
64 NGKPKGRKATVTDSSRTAYVQVRSRSLTSBDSAVYFCAKENRDERGYAMDYWGQFTV 123
116 TVSSAKTPKLGG-----DIELTQSPKPMSTSVDRLVNTYKASQNTGTVNWAFOQPG 169
Db 124 TVSSGGGSGCCGCGGCCNNIQLQTSPMSMSTSVDRLVNTYKASQNTGTVNWAFOQPG 183
QY 170 QSPKVLIYSASYRSYGVPDFGTGGSGTDFLTATISNVOSEDLEYFCQQHTYPLTFCGG 229
Db 184 QSPKLITIWASTRHTGVPDFGTGGSGTDFLTATISNVOSEDADYFCQQSSXPWTFCGG 243

FILING DATE:	28-JAN-1993	Qy	61 NYNEFKGKATVTAATSSRTPAYQVRSITSEDSAVYFCARSASWYFPDVWGARTTVSSA 120
ATTORNEY/AGENT INFORMATION:		Db	120 NYSETFKRATLTVTWSNTSYMOSSLTEDEDTAYFCARGVG--LDYWGCGTTVSSG 177
NAME: Smith Ph.D., Julie K.		Qy	121 KTPPKLGG-----DELTOSPKEMTSVGDRTTAKSONGVNTYKASQNGTNVAWFQOKPGSKV 174
REGISTRATION NUMBER: P-38,619		Db	178 GGGGGGGGGGGSDIELTQSPNSLSTSIGIRIITCKASQDVDTAVGYQRPQGSPL 237
REFERENCE/DOCKET NUMBER: ST92006-US		Qy	175 LIYSASYRYSGVPDRFTGSGSGTDFTLTISNQSEDLAEYFCQOHTYPLTFGGTLEI 234
TELECOMMUNICATION INFORMATION:		Db	238 LIFWSSSTRATCVPDRFTGSGSGTDFTLTISNQSEDLAFCHQISSYPFTFGSTYLEI 297
TELEPHONE: (610) 454-3839		Qy	235 KRADAAAG 243
TELEFAX: (610) 454-3808		Db	298 KR---RAAG 303
SEQUENCE CHARACTERISTICS:			
LENGTH: 249 amino acids			
TYPE: amino acid			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
US-11-146-077-18			
Query Match Score 61.8%; DB 6; Length 249;			
Best Local Similarity 69.5%; Pred. No. 1.2e-57; Indels 13; Gaps 2;			
Matches 171; Conservative 22; Mismatches 40; Indels 13; Gaps 2;			
RESULT 13 US-10-511-794-21			
Query Sequence 21, Application US/10511794			
Publication No. US20050158322A1			
GENERAL INFORMATION:			
APPLICANT: Center for Genetic Engineering and Biotechnology			
TITLE OF INVENTION: ANTIBODY FRAGMENTS SPECIFIC FOR HUMAN CARCINOEMBRYONIC			
TITLE OF INVENTION: ANTIGEN (CEA)			
FILE REFERENCE: 976-20 PCT/US			
CURRENT APPLICATION NUMBER: US/10/511,794			
CURRENT FILING DATE: 2004-10-19			
PRIOR APPLICATION NUMBER: PCT/CU2003/000005			
PRIOR FILING DATE: 2003-04-28			
PRIOR APPLICATION NUMBER: CU2002/00886			
PRIOR FILING DATE: 2002-04-09			
NUMBER OF SEQ ID NOS: 21			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO: 21			
LENGTH: 255			
TYPE: PRT			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: diabody MS			
US-10-511-794-21			
Query Match Score 61.4%; DB 5; Length 255;			
Best Local Similarity 65.2%; Pred. No. 3.4e-57; Mismatches 27; Indels 13; Gaps 5			
Matches 172; Conservative 27; Mismatches 27; Indels 13; Gaps 5			
RESULT 14 US-10-096-246-36			
Sequence 36, Application US/10096246			
Publication No. US20030100060A1			
GENERAL INFORMATION:			
APPLICANT: Her Majesty the Queen in right of Canada, as represented by the Minister of National Defence			
APPLICANT: Nagata, Leslie P			
APPLICANT: Fulton, R. Blaine			
APPLICANT: Hu, Weigang			
APPLICANT: Alvi, Azhar Z			
TITLE OF INVENTION: No. US2004005333A1el Fusion Protein of Human IgG1 Heavy Chain Co			
TITLE OF INVENTION: Antibody Against Venezuelan Equine Encephalitis Virus			
FILE REFERENCE: NEH-0013			
CURRENT APPLICATION NUMBER: US/10/378,832A			
CURRENT FILING DATE: 2003-03-05			
NUMBER OF SEQ ID NOS: 2			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO: 2			
LENGTH: 622			
TYPE: PRT			
ORGANISM: mouse hybridome cells and human lymphocytes			
US-10-378-832A-2			
Query Match Score 61.8%; DB 4; Length 622;			
Best Local Similarity 68.7%; Pred. No. 3.1e-57; Mismatches 24; Indels 11; Gaps 3;			
Matches 171; Conservative 24; Mismatches 43; Indels 11; Gaps 3;			
RESULT 14 US-10-096-246-36			
Sequence 36, Application US/10096246			
Publication No. US20030100060A1			
GENERAL INFORMATION:			
APPLICANT: The Minister of National Defence, Government of Canada			
1 MAQVOLQSGAELVRPGTSVKISKACKASGYTFNWLGYKQRDPGHLWIGDLYPGGGYT 60			
60 MAQVOLQSGPVELVKPGASKVSKISKACKASGYTFNWLGYKQRDPGHLWIGDLYPGGGYT 119			

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 9, 2006, 03:55:47 ; Search time 19.0991 Seconds
(without alignments)
180.014 Million cell updates/sec

Title: US-10-049-404-2

Perfect score: 1395

Sequence: 1 MAQVOLQQSAELVRPGTSV.....GSEQQLISBDLNSHHHHH 262

Scoring table: BLOSUM62

Gappen: 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /cgns2_6/podata/2/pubpaas/us08_new_pub.pep;
2: /cgns2_6/podata/2/pubpaas/us05_new_pub.pep;
3: /cgns2_6/podata/2/pubpaas/us07_new_pub.pep;
4: /cgns2_6/podata/2/pubpaas/pct_new_pub.pep;
5: /cgns2_6/podata/2/pubpaas/us05_new_pub.pep;
6: /cgns2_6/podata/2/pubpaas/us10_new_pub.pep;
7: /cgns2_6/podata/2/pubpaas/us11_new_pub.pep;
8: /cgns2_6/podata/2/pubpaas/us60_new_pub.pep;

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	805.5	57.7	615	US-10-512-184-50	Sequence 50, App1	
2	800	57.3	290	US-11-032-773-957	Sequence 957, App	
3	793.5	56.9	543	US-10-495-164-3	Sequence 3, App1	
4	790.5	56.7	319	US-11-032-773-955	Sequence 955, App	
5	779	55.8	269	US-10-839-799-109	Sequence 199, App	
6	765.5	54.9	245	US-11-054-515-1902	Sequence 1902, App	
7	763.5	54.7	251	US-11-054-515-1921	Sequence 1921, App	
8	760.5	592	6	US-10-016-686-4	Sequence 4, App1	
9	759	54.4	248	US-11-054-515-1778	Sequence 1778, App	
10	757	54.3	248	7	US-11-054-515-1008	Sequence 1008, App
11	755.5	54.2	243	6	US-10-016-686-1	Sequence 1, App1
12	755.5	54.2	247	7	US-11-054-515-3242	Sequence 3242, App
13	751.5	53.9	488	6	US-10-016-686-3	Sequence 3, App1
14	748	53.6	242	7	US-11-054-515-1915	Sequence 1915, App
15	747	53.5	244	7	US-11-054-515-1881	Sequence 1881, App
16	745	53.4	248	7	US-11-054-515-1446	Sequence 1446, App
17	741.5	53.2	249	7	US-11-054-515-926	Sequence 926, App
18	738	52.9	250	7	US-11-054-515-932	Sequence 932, App
19	737.5	52.9	249	7	US-11-054-515-918	Sequence 918, App
20	736	52.8	248	7	US-11-054-515-1104	Sequence 1104, App
21	734	52.6	246	7	US-11-054-515-1920	Sequence 1920, App
22	731.5	52.4	241	7	US-11-054-515-1577	Sequence 1577, App
23	731.5	52.4	249	7	US-11-054-515-1635	Sequence 1635, App
24	728.5	52.2	249	7	US-11-054-515-919	Sequence 919, App
25	728	52.2	248	7	US-11-054-515-177	Sequence 177, App

ALIGNMENTS

RESULT 1
US-10-512-184-50

; Sequence 50, Application US/105121844
; Publication No. US20050244901A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
; TITLE OF INVENTION: Antibodies recombinant antibodies recombinant
; antibody fragments and fusions mediated plant disease
; TITLE OF INVENTION: resistance against fungi.
; FILE REFERENCE: 1581.01US01
; CURRENT APPLICATION NUMBER: US/10/512,184
; CURRENT FILING DATE: 2004-10-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 50
; LENGTH: 615
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
; OTHER INFORMATION: - cmyc/His6.

US-10-512-184-50

Query Macch 57.7%; Score 805.5; DB 6; Length 615;
Best Local Similarity 59.6%; Pred. No. 2.1e-48;
Matches 165; Conservative 35; Mismatches 58; Indels 19; Gaps 6;

Qy 1 MAQVOLQSSAELVRPGTSVYKISKASAGTFTNWLGWVQRPGLWIGDIYPCGGYT 60
Db 342 MAQVOLQSSGTIVLARGASTKMSCKASGTTSTMWVQRPGLEWIGAIYFCNSDT 401

Qy 61 NYNEEFKGKATVYADTSSRVAVYQVSLSEDSAYFCARSASVYF- DYGARTRTVVS 118
Db 402 SYNQKFKGKAKLTAVTSTAYMFLSLNEDSAYVCTPT-DWDIAMDWTGQTSTVTVS 460

Qy 119 SAKT-----TPKLGGDIELTQS PKFMSTS VGD RNVTVYKASQNYTGNTVWAFQOK 167
Db 461 SGTSGSKGPKGEGSTKGA PDI LFQSPYTMASASPEK YVMTCSASSV-NYI WYQWK 519

Qy 168 PGQSPKVLVYSASTRYSGVDPDRFTSGSGDFLTITISVNOSED L AYF CQOYHTPLT F 227
Db 520 SGTPSKRWPIDTSKLASGVPRFGSGSGTSFSLTISSMAEDIATYCCQWSSPPLTFG 579

Qy 228 GGTKLKEIKRADAAGAAGSEQKLISEEDLNS--HHHHHH 262
Db 580 AGTKLKEIKRADA - EQLISEBDLGALDHHHHH 614

US-10-495-064-3	OTHER INFORMATION: protein construct
Qy	Query Match 56.9%; Score 793.5; DB 6; Length 543; Best Local Similarity 59.1%; Pred. No. 1.2e-47; Indels 31; Gaps 4; Matches 162; Conservative 26; Mismatches 55;
Db	3 OVOLOQSGAELVYRPGTSVKISCKASKAGTFTNTNWLGWIKORPGHGLEWIGDIPCGGGTYTN 62 287 QVLOQSGPVELVKPGASVKISCKASGAFSRSWNWIKORPGGLEWIGRIPEGDGDTNY 346
Qy	63 NEKFKGKATVADTSSRTAYQVQRSLTSESDAVFCARS---ASWYFDWGRARTTVS 118 Db 347 NGKFKGKATLADKSSSTAYMQSSLTSESDAVFCARGNTVUVPYTMDWGQGTTVTS 406
Qy	119 SAKTTPKLGG-----DIETLSPKFMSTSVGDRVNNTYKASQN----GTNVAWFQKQP 168 Db 407 SGCGSGGGGGGGGGSDIETLQPSALSVLGRATISCRASESDVSKNSFMEWYQKQP 466
Qy	169 GQSPKVLIYASRYSGVPDRENGSGSGTDFTLTISVNOSEDLAEYFCQQYHTYPLTFGG 228 Db 467 GQPKLILYASNLSEGYPARFSGSGSRDFTLTIDPVEEADDAACTYCCOONNEDPLTFGG 526
Qy	229 GTKLEIRKADAAGSBOKLISEEDLNSHHHHHH 262 Db 527 GTKLELRKAAG-----HHHHHHH 543
RESULT 4	
US-11-032-773-955	
Sequence 955, Application US/11032-773-955	
; Publication No.: US20060018911A1	
; GENERAL INFORMATION:	
; APPLICANT: Ault-Riche, Dana	
; ATTORNEY: Levy, Ronald	
; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS	
; FILE REFERENCE: 17102-013001 / 1762	
; CURRENT APPLICATION NUMBER: US/11/032_773	
; CURRENT FILING DATE: 2005-01-11	
; PRIOR APPLICATION NUMBER: 60/536,184	
; PRIOR FILING DATE: 2004-01-12	
; PRIOR APPLICATION NUMBER: 60/557,591	
; PRIOR FILING DATE: 2004-03-29	
; NUMBER OF SEQ ID NOS: 958	
; SOFTWARE: FastSEQ for Windows Version 4.0	
; SEQ ID NO: 955	
; LENGTH: 319	
; TYPE: PRT	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: pBAD S1C5 CD20 His Protein Sequence	
US-11-032-773-955	
Qy	Query Match 56.7%; Score 790.5; DB 7; Length 319; Best Local Similarity 53.4%; Pred. No. 1.2e-47; Indels 59; Gaps 7; Matches 171; Conservative 31; Mismatches 59;
Db	1 MAQVQLQSGAELVYRPGTSVKISCKASKAGTFTNTNWLGWIKORPGHGLEWIGDIYPGGYT 60 1 MAEVQQLQSGAELVTKPGASVKISCKASGFTDVLHWYKQRPEGLETFGISPGNDI 60
Qy	61 NYNEKFGRATVADTSSRTAYQVQRSLTSESDAVFCARSASH---YFDWGRARTVT 116 Db 61 RYNEKFGRATLADKSSSTAYQLNLSLTSESDAVFCRSFYYDDNQGDYWGQGTTLT 120
Qy	117 VSSAKTPKLGG-----DIELTOSPKFMSTSVGDRVNNTYKASQNVTN-VAWF 164 Db 121 VSSS-GAIGGGSGKGGSGGSSIVLTSPPAMSASSLERVMTCTASSVSSSS-FHWY 179
Qy	165 QQPKGQSPKVLIYASRYSGVPDRENGSGSGTDFLTISVNOSEDLAEYFCQQYHTYPL 224 Db 180 QQPKGSPKVLIYTTSSNLASGVAPAREGGSGSYSLTISVMEADAATYCHQTHRSPL 239

		RESULT 5		
Qy		US-10-839-799-109		
		Sequence 109, Application US/10839799		
		Publication No. US20050249726A1		
		GENERAL INFORMATION:		
		'APPLICANT: OHTOMO, Toshihiko SATO, Koh		
		TSUCHIYA, Masayuki TITLE OF INVENTION: RESPIRATORY HUMAN ANTIBODY TO HUMAN MEDULLOBLASTOMA CELLS		
		NUMBER OF SEQUENCES: 132		
		CORRESPONDENCE ADDRESS: ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA		
		ZIP: 20007-5109		
		COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS		
		SOFTWARE: PatentIn Release #1.0, Version #1.30		
		CURRENT APPLICATION DATA: APPLICATION NUMBER: US/10/839,799 FILING DATE: 06-May-2004 CLASSIFICATION: <Unknown>		
		PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/646,265 FILING DATE: 09-SEP-1996 APPLICATION NUMBER: WO PCT/JP94/01763 FILING DATE: 19-OCT-1994 APPLICATION NUMBER: JP 5-291078 FILING DATE: 19-NOV-1993 ATTORNEY/AGENT INFORMATION: NAME: WEGNER, Harold C. REGISTRATION NUMBER: 25,258 REFERENCE/DOCKET NUMBER: 533466/184		
		TELECOMMUNICATION INFORMATION: TELEPHONE: (202)672-5300 TELEFAX: (202)672-5399 TELEX: 904136		
		INFORMATION FOR SEQ ID NO: 109: SEQUENCE CHARACTERISTICS: LENGTH: 269 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 109:		
		US-10-839-799-109		
Qy		Query Match 55.8%; Score 779; DB 6; Length 269; Best Local Similarity 61.8%; Pred. No. 6.4-e-47; Matches 149; Conservative 35; Mismatches -51; Indels 6; Gaps 1		
Db		1 MAQQVQLOQSGABLRPGTSVKISKCKASGYTFNLYWLGKXQRPGLEWIGDLYPGGGXT 60 21 MAQVQLVSGAEVKKPPSSVKVCKASGFNTIKDTVTIHWVRQAPGQGLEWGRIDPADGNT 80		
Qy		61 NYKEPKFGKATVADTSRTAVYQVRLTSEPSAVYFCAREASAWFDWGMARTTVSSA 124 Db		81 KYDPKFGQRTVITADEBNTIAVMEPLLRSRDTAFYCASAAYVNODYNGQTITVSSG 141
Qy		125 YTTMPKFGG-----DIBUTOSPKEMTSVGDVRVNTYKASONGTGNVWFOOKPGOSPKV 174		


```

; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1778
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1778

Query Match      54.4%; Score 759; DB 7; Length 248;
Best Local Similarity 59.3%; Pred. No. 1.4e-45;
Matches 147; Conservatve 37; Mismatches 50; Indels 14; Gap 1

Qy   3 QVQLQSSAELVRPGTSRKVSKASGYTTNYLGWVQRPGEGLWIDIVPGGGVYI
Db   1 QVQLQSSAEVRKPGASRKVSKASGYFTSYGSWVQAPGLEMNGWI SAYNGNTT

Qy   63 NEFKFGKATVTAITSSRPAVQVRSLSATVFCARS----ASWY---FDYWGAR
Db   61 AQKLQGRMTMTDTSTAYMEILRSLSRDATVYCASSYYDLTGTYPFPGMDWVGCKC

Qy   115 VTISSAKTTPKLGG----DIELTQSPKFMSTSVGDVRNVTYKASQNVTGNTVAFQG
Db   121 VTYSGGCGSGGGCGGGCGSIDIQMTQSPSTLSASIGDRVTITCRASEGIYHNLAWYQQ

Qy   169 GQSPBKVLTYAISTRYGVDRFTCSGSDFFTISNSQSEDLABYFCQOHTYPLTF
Db   181 GKAFLLIIYKASSLASGAPSRSFSGSGSGTDFLTISSLQPDFPATYYCQOQSNYPLTF

Qy   229 GTKLEIKR 236
Db   241 GTKLEIKR 248

RESULT 10
US-11-054-515-1008
; Sequence 1008, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS/3P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/233,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1008
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-1008

```

RESULT 12

US-11-054-515-3242

Sequence 3242, Application US/11054515

PUBLICATION NO. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2000-10-17

Remaining prior application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3242

SEQ ID NO 3

LENGTH: 488

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: deduced amino acid sequence for the B7-1.5T4.1 fusion protein

US-10-016-686-3

Query Match Score 54.2%; DB 7; Length 247;

Best Local Similarity 58.7%; Pred. No. 2.4e-45; Mismatches 38; Indels 13; Gaps 2;

Db 486 EIK 488

Query Match Score 53.9%; DB 6; Length 48;

Best Local Similarity 61.7%; Pred. No. 8.3e-45; Mismatches 28; Indels 9; Gaps 2;

Db 246 SEVQLQQSSPDLYKPGASVKISKASGTYFTWLGWYKQRPHGLEMGIDYPGGGYTIN 61

Qy 2 AYVOLQGSSAELYRPGTSEVKSISKAQSGTYFTWLGWYKQRPHGLEMGIDYPGGGYTIN 61

Db 246 YNEBFKGKATVTTADTSRSTAYVQVRLTSEDSAVYFCARS---ASWYFDVWGRARTTVVS 118

Qy 62 YNEBFKGKATVTTADTSRSTAYVQVRLTSEDSAVYFCARS---ASWYFDVWGRARTTVVS 118

Db 306 YNQKPFKDQKALITYDKSSTTAKSLSLTSEDSAVYFCARSMTMNYDVGOTSVTSV 365

Qy 119 S----AKTPKUGGDIELQDPKFEMTSVGRVNTYKASQNVGTVNWAFQOKPGQSP 172

Db 366 SGGGSGGGTGGGGSSIVWTQTPFLVSGAGRVTICKASQVSNDVWAFQOKPGQSP 425

Qy 173 KVLLIYASRYSTRGVPDRFTGSGSTDFTLTISVQSEDIAEYFCQQTPLFQGGGKL 232

Db 426 TLLISYTSRYYAGVPDRFIGSGTDFITISQEDVAYFCQDYNSSPPFGGTMKL 495

RESULT 14

US-11-054-515-1915

Sequence 1915, Application US/11054515

PUBLICATION NO. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

FILE REFERENCE: PFS23P3

CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10

PRIOR APPLICATION NUMBER: 60/543,296

PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347

PRIOR FILING DATE: 2004-06-18

PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: US-10-016-686-3

Sequence 3, Application US/10016686

PUBLICATION NO. US200601422A1

GENERAL INFORMATION:

; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO: 1915
 ; LENGTH: 242
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-054-515-1915

Query Match 53.6%; Score 748; DB 7; Length 242;
 Best Local Similarity 59.9%; Pred. No. 7.6e-45; Indels 8; Gaps 2;
 Matches 145; Conservative 37; Mismatches 52; Gaps 2;

Qy	3 QVQLOQSGAELVRPGTSVKISCKASGYTPTNYWLGWYKQRPGHGLEWIDIYPGGGTYNY 62
Db	1 QVQLOQSGAELVRPGTSVKISCKASGYTPTNYWLGWYKQRPGHGLEWIDIYPGGGTYNY 60
Qy	63 NEKFKGKATVTADTSRATAYQVQRLSTSVDAYFCAR-SASWY--FDVWGAETTVTVS 118
Db	61 AQKFQGRVITADKSTSTAYMELSSLRSDTAVTCARDGSYYDADIWGKGTMVTVS 120
Qy	119 SAKTPKLGG-----DIELTOSKPKFMSVGDVNNTYKASQNVGTNAYWFQOKPGQSP 172
Db	121 SGCGSGGGGGGGSDIMTQSSTLSAVGDVITCRASQISSWLAQOKPGKAP 180
Qy	173 KVLYIASTRYSGPDRFTSGSGTDFLTISNQSEDLAEYFCQOYHTYPLTFGGGTVKL 232
Db	181 KLLIYASSLQSGTPSRFSGSGTDFLTISNQSEDPAITYCQQANSFPLTFGGGTVK 240
Qy	233 EIKR 236
Db	241 EIKR 244

Search completed: February 9, 2006, 04:00:31
 Job time : 20.0991 secs

Query Match 53.6%; Score 748; DB 7; Length 242;
 Best Local Similarity 59.9%; Pred. No. 7.6e-45; Indels 8; Gaps 2;
 Matches 145; Conservative 37; Mismatches 52; Gaps 2;

Qy	63 NEKFKGKATVTADTSRATAYQVQRLSTSVDAYFCAR-SASWY--FDVWGAETTVTVS 120
Db	61 AQKFQGRVITADKSTSTAYMELSSLRSDTAVTCARDGSYYDADIWGKGTMVTVS 120
Qy	121 KTPPKLGG-----DIELTOSKPKFMSVGDVNNTYKASQNVGTNAYWFQOKPGQSP 174
Db	121 GGCGSGGGGGSDIQMTQPSFUSAVGDVITCRASQINNNLYWFQOKPGQSPKL 180
Qy	175 LIYASRYSGVVPDRFTSGSGTDFLTISNQSEDLAEYFCQOYHTYPLTFGGGTVKL 234
Db	181 LIYASSLQSGTPSRFSGSGTDFLTISNQSEDPAITYCQDSDYPLTFGGGTVKL 240
Qy	235 KR 236
Db	241 KR 242

RESULT 15
 US-11-054-515-1981
 Sequence 1881, Application US/11054515
 Publication No. US20050255532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PFS23P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293,499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO: 1881
 LENGTH: 244
 TYPE: PRT

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Copyright	GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd.	
Run on:	February 9, 2006, 03:18:06 ; Search time 281.675 Seconds (without alignments) 425.847 Million cell updates / sec	
Title:	US-10-049-404-3	
Perfect Score:	1470	
Sequence:	1 MAQVQLQQSGAQLARPGASV.....GSEQLLISEEDINHHHHH 273	
Scoring table:	BLOSUM62 Gapext 10.0 , Gapext 0.5	
Searched:	2443163 seqs, 439378781 residues	
Number of hits satisfying chosen parameters:	2443163	

ALIGNMENTS

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : A_Geneseq_21:
 1: GeneseqP19908: *
 2: GeneseqP19908: *
 3: GeneseqP20008: *
 4: GeneseqP20018: *
 5: GeneseqP20028: *
 6: GeneseqP2003ab: *
 7: GeneseqP2003bs: *
 8: GeneseqP20048: *
 9: GeneseqP20058: *

RESULT 1
 AAB70763
 ID AAB70763 standard; protein; 273 AA.
 XX
 AC AAB70763;
 AC
 XX (first entry)
 DT 18-MAY-2001
 XX
 DE Single chain Fv antibody construct anti-CD30 VL domain protein.
 XX
 KW Single chain Fv antibody; anti-CD16; anti-CD30; VH domain; VL domain;
 KW fusion construct; CD16 receptor; CD30 surface protein; cytostatic;
 KW tumor cell; natural killer cell activation; Hodgkin's disease;
 KW Reed-Sternberg disease.

130

Result No.	Score	Query		Length	DB	ID	Description
		Match	Start				
1	1410	100.0	273	4	AAB70753		Aab70753 Single ch
2	1231.5	83.8	272	7	ADE29203		Ade29203 Multivale
3	1041.5	70.9	415	2	AAR56484		Aar56484 SCFV PRAS
4	1027.5	69.9	402	2	AAR56485		Aar56485 SCFV PRAS
5	1026.5	69.8	269	2	AAR54756		Aar54756 SCFV PRAS
6	1025.5	69.8	269	2	AAR56482		Aar56482 SCFV PRAS
7	1015.5	69.9	256	2	AAR25668		Aar25668 SCFVB18 C
8	1014.5	69.0	256	2	AAR25884		Aar25884 SCFVB18 C
9	1014.5	69.0	435	2	AAR56483		Aar56483 SCFVB18 C
10	1011.5	68.8	256	2	AAR25882		Aar25882 SCFVB18 C
11	1010.5	68.7	428	2	AAW24027		Aaw24027 Single ch
12	1010.5	68.7	443	2	AAW24025		Aaw24025 Single ch
13	1009.5	68.7	256	2	AAR2587		Aar2587 SCFVB18 C
14	1009.5	68.7	256	2	AAR2585		Aar2585 SCFVB18 C
15	1008.5	68.6	256	2	AAR2586		Aar2586 SCFVB18 C
16	1005.5	68.4	256	2	AAR2583		Aar2583 SCFVB18 C
17	862	58.6	562	6	ABR57059		Abr57059 Plasmid F
18	834.5	56.8	239	8	ADTO7625		Adt07625 Polypept F
19	825	56.1	248	2	AAW58826		Aaw58826 Human CPD
20	824.5	56.1	288	2	AAW82317		Aaw82317 Mouse b1
21	821.5	56.1	288	2	AAM82316		Aam82316 Mouse OKM
22	821.5	55.9	243	8	ADTO7627		Adt07627 Polypept F
23	807.5	54.9	288	2	AAW82482		Aaw82482 Mouse b1
24	799.5	54.9	539	3	AAV50823		Aav50823 Fv-antipept

or Red-Sternberg diseases. (1) have a stronger lytic action than known specific antibodies, can be produced on a large scale with high purity and contain no components that can induce unwanted immune responses

Sequence 273 AA:

```

Query Match      100.0%; Score 1470; DB 4; Length 273;
Best local Similarity 100.0%; Pred. No. 4.2e-93;
Matches 273; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

```

Qy	Ddb	1	MAQVLOQSGAELRPGASVYMSCKASGIFTFTTIIHWVRQRPHDLEWGYINPSSGTS	60
Qy	Ddb	1	MAQVLOQSGAELRPGASVYMSCKASGIFTFTTIIHWVRQRPHDLEWGYINPSSGTS	60
Qy	Ddb	61	DYNQFKGKTTILADKSSNTAYMQLNSLTSEDSAVYCARRADGNYETWTAWGQGT	124
Qy	Ddb	61	DYNQFKGKTTILADKSSNTAYMQLNSLTSEDSAVYCARRADGNYETWTAWGQGT	124
Qy	Ddb	121	VTVSSEAKTTPKLGCDIQAVVTSALTTSGETVTLTCRSNTGTVTSNANWYQEKPDH	184
Qy	Ddb	121	VTVSSEAKTTPKLGCDIQAVVTSALTTSGETVTLTCRSNTGTVTSNANWYQEKPDH	184
Qy	Ddb	181	LFTGLIGHTNNRAPEVPAFSGSLIGDKAALTTGAQTEDEAIYFCALWYTNHVFGGGT	24
Qy	Ddb	181	LFTGLIGHTNNRAPEVPAFSGSLIGDKAALTTGAQTEDEAIYFCALWYTNHVFGGGT	24
Qy	Ddb	241	KLTIVLGQPKSAAAGSSEQKLISEEDLNSHHHHH	273
Qy	Ddb	241	KLTIVLGQPKSAAAGSSEQKLISEEDLNSHHHHH	273

RESULT 2
ADE29203 ADE29203 Standard; protein: 272 AA.

22203; JAN-2004 (first entry) Bivalent multimeric antibody CD19xCD16 related protein 3. Bivalent multimeric antibody; bispecific diabody; BsDb; an B cell marker; CD19; human Fcgamma receptor III; CD16; cytosatic; non-suppressive; B-cell malignancy; non-Hodgkin lymphoma; B-cell mediated autoimmune disease; B-cell depletion; immune response; an anti-murine antibody response; CD19 x CD16 BsDb; PSKD19x16; mouse

Location/Qualifiers	
31. .35	/label= Complimentarity_determining_region_H1
50. .66	/label= Complimentarity_determining_region_H2
99. .113	/label= Complimentarity_determining_region_H3
124. .133	/label= Synthetic_linker
158. .171	/label= Complimentarity_determining_region_L1
187. .196	/label= Complimentarity_determining_region_L2
226. .234	/label= Complimentarity_determining_region_L3
255. .264	/label= C-myc_epitope
267. .272	/label= C-myc_epitope
278. .284	/label= C-myc_epitope
291. .297	/label= C-myc_epitope

XX 14-NOV-2001; 2001EP-00127061.
PF
XXX
PR 14-NOV-2001; 2001EP-00127061.

XX PA (AFFILIATE) AFFINITY THERAPEUTICS AG.
XX PA Kiprivanov MS. Moldenhauer G.
XX Le Gall F. Moldenhauer G.
Little M. Cochlovius B.

P1	Schaerer JH;
XX	WPI; 2003-620028/59.
DR	N-PSDB; ADE29-01.
XX	Multivalent multimeric antibody for treating B-cell malignancies such as non-Hodgkin lymphoma, comprises specificities, and antigen-binding domain
PT	PT specific to human CD19 and CD16
PT	PT non-specific

AA Example 1; SEQ ID NO 3; 38pp; English.
PS

This invention relates to a novel multivalent multimeric antibody (a bispecific dAbody - BsdB) which comprises at least two binding sites specific for the human B cell marker CD19 and human Fc gamma receptor III (CD16). The invention may allow the development of compositions with cytostatic or immunosuppressive activity. The antibody is useful for the diagnosis and treatment of B-cell malignancies such as non-Hodgkin lymphoma, B-cell mediated autoimmune diseases or the depletion of B-cells. The multivalent multimeric antibody avoids the undesired immune response such as human anti-murine antibody response. The specification provides a process for stable high yield of recombinant antibodies. The present sequence is that of a mature mouse derived protein encoded by the DNA sequence of the CD19 x CD16 FsdB in the expression plasmid pSKD19x6 which was used in the exemplification of the invention.

Sequence 272 AA;

```

Query Match          83.8%;  Score 121.5;  DB 7;  Length 272;
Best Local Similarity 83.7%;  Pred. No. 1e-16;
Matches 234;  Conservative 14;  Mismatches 22;  Indels 3;  Gaps 2

```

Qy	Db
3	QVQLQSGAELRPGASVMSKCSGYTTTHTWQRPGHLEWIGYINPSGSYD
1	QVQLQSGAELVRPGCSSVKISKCSGYAFSSYYNNWWKRPGQCLEWIGQIwGDGDTNY

Qy	Db
63 NQNPKGKTTLTADDESSNTAYMOLNSLTSDAVYTCARR - ADGYNNEYXTWFAWGQQT	12.9
61 NGKPKGKALTLTADDESSNTAYMOLNSLASESDAVY	11.9

Qy	Db
121	VTVSAAKTPKLGGDIOAVVTOESALTTSPGETTLTCSRNTGTVVTSNYANVWQEKPDH
120	VTVSAAKTPKLGGDIOAVVTOESALTTSPGETTLTCSRNTGTVVTSNYANVWQEKPDH

Qy	Db
181 LFTGJLGHNTNRAPEVPAFSGSLJDGXALTTGAQTEDEAYFCALWYNNHWFGGGT	24
180 LFTGJLGHNTNRAPEVPAFSGSLJDGXALTTGAQTEDEAYFCALWYNNHWFGGGT	2395

Qy	Db
241 KLTTVQGPISAAAGSEQLISEEDLNSHHHHH	273
240 KLTTVQGPISAAAGSEQLISEEDLNSHHHHH	272

XX AAR 56484 ;
AC XX 25. MAY 2003
DP (Received)

DT 26-MAR-1995 (first entry)
 XX
 DE SCFV PRAS109 and PRAS113.
 XX
 KW Amplification; single chain variable region fusion protein; PCR.

PR	10-JUL-1990;	90GB-00015198.	XX	AAR56483;
PR	19-OCT-1990;	90GB-00022845.	AC	
PR	12-NOV-1990;	90GB-00024503.	XX	
PR	06-MAR-1991;	90GB-00024503.	DT	25-MAR-2003 (revised)
PR	15-MAY-1991;	90GB-00004744.	DT	26-MAR-1995 (first entry)
XX			XX	
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.	ScFv PRAS108 and PRAS112.	DB	
PA	(MEDI-) MED RES COUNCIL.	Amplification; single chain variable region fusion protein; PCR.	XX	
XX			XX	
PI	McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;	XX	XX	
PI	Jackson RH, Holliger KP, Marks JD;	OS	Synthetic.	
XX			XX	
DR	WPI; 1992-056862/07.	PN		
DR	N-PSDB; AAQ23860.	WOA15644-A1.		
XX			XX	
PR	Producing members of specific binding pairs - by expression in recombinant host cells with a secretting replicable genetic display package.	PD	21-JUL-1994.	
PR		PF	17-JAN-1994;	94WO-GB0000087.
XX		XX	XX	
PS	Example 38; Fig 44; 209pp; English.	PR	15-JAN-1993;	93GB-00000686.
XX		XX	XX	
CC	The sequence is encoded by an antibody scFv fragment directed against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and IV chains of an MAb against NP were separately amplified and reassembled to form the construct, which was then ligated into the fd gene 111 contg. vector, fdCAT2, derived from fdPv/Xb. (See AAQ21095). The clone having the scFvB18 sequence fused in frame to gene 111 was designated fdCAT2 with the tet gene replaced by a kanamycin resistance gene. (See AAQ218). Alternatively the fragment was cloned into fdOGKan (fdCAT2 with the tet gene replaced by a kanamycin resistance gene) to give fdOGKanscFvB18, or into the phagemid pHEN1 to create pHEN1-scFvB18. The constructs were used to test the effect of using mutator strains to increase the diversity of the cloned genes. The strains NR9046 mutD5: fN10 and NR9046mutT1: fN10 were constructed. After 4 rounds of mutation and screening, 40 phage inserts were sequenced. They each displayed single mutations in 6 different positions, five being in the light chain region. More than 70% of the mutations occurred at positions 724 and 725 (of the nucleotide sequence) changing the first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in 3 cases). The mutant shown here occurred once. The mutant fragments had affinities for NP which were comparable to the wild-type scFv fragment (20nm). N.B. fdCAT2 is also referred to as fd-tet-DOG1 and fdDOG1. See also AAR21260-307, 309-311; AAR22450, 565-581	PS	Disclosure; Fig 9; 114pp; English.	
CC		XX	XX	
CC	The sequence is that of the ScFv PRAS108 and PRAS112 between HindIII and EcoRI site obtd. by PCR. See also AAR56482-5. (Updated on 25-MAR-2003 to correct PN field.)	CC	CC	
XX		XX	XX	
SQ	Sequence 435 AA;	CC	Sequence 435 AA;	
Qy	1 MAQVQLQSGAELAARGASVNRNSKASCGTYFTTTIHWYRQRPHDLEWIGVNPSSSY 60	Query Match 69.0%; Score 1014.5; DB 2; Length 435;	Qy	1 MAQVQLQSGAELAARGASVNRNSKASCGTYFTTTIHWYRQRPHDLEWIGVNPSSSY 60
Db	21 MAQVQLQSGAELAARGASVNRNSKASCGTYFTTTIHWYRQRPHDLEWIGVNPSSSY 80	Best Local Similarity 74.2%; Pred. No. 1.e-61;	Db	21 MAQVQLQSGAELAARGASVNRNSKASCGTYFTTTIHWYRQRPHDLEWIGVNPSSSY 80
Qy	2 AYVOLQSGAELAARGASVNRNSKASCGTYFTTTIHWYRQRPHDLEWIGVNPSSSY 61	Mismatches 20; Conservative 20; Mismatches 22; Mismatches 21;	Qy	61 DYNQNFKGKTTLTDAKSSNTAYMQLNSLTSEDSAVYCARADDYGNVETWFAVGQGTT 120
Db	62 YNQNFKGKTTLTDAKSSNTAYMQLNSLTSEDSAVYCARADDYGNVETWFAVGQGTT 65	Indels 7; Gaps 3;	Db	81 KYNKEFKSKATLTVDKPSSTAYMQLSSLTSEDASAVYCAR--YYDYGSSYFPWGQGTT 137
Qy	62 YNQNFKGKTTLTDAKSSNTAYMQLNSLTSEDSAVYCARADDYGNVETWFAVGQGTT 121	Qy	121 VTVS---AKTPKLGGDIQAVTQESALITSPGETVTLCRSNTGVTTSNYANVQE 176	
Db	66 YNEKFKSKATLTVDKPSSTAYMQLSSLTSEDASAVYCA-RYDGSSY--FDWQGQTTV 122	Db	138 VTVSGGGGGGGGGGGGGSOAVTQESALITSPGETVTLCPSTSIGAVTTSNYANVQE 197	
Qy	122 TVSS---AKTPKLGGDIQAVTQESALITSPGETVTLCRSNTGVTTSNYANVQE 177	Qy	177 KPDHLFTGLIGHTNRAFGVPARSGSLIGDKAALTGAQTEDAEYFCALWNNHVSF 236	
Db	123 TVSSGGGGGGGGGGGGSOAVTQESALITSPGETVTLCRSSTGATTTSNYANVQE 182	Db	198 KPDHLFTGLIGHTNRAFGVPARSGSLIGDKAALTGAQTEDAEYFCALWNNHVSF 257	
Qy	178 PDHLFTGLIGHTNRAFGVPARSGSLIGDKAALTGAQTEDAEYFCALWNNHVSF 237	Qy	237 GGCKLTVLGQPKSAAAGSEOKLJSEEDLNS 267	
Db	183 PDHLFTGLGGTNNRAPGVPARSGSLIGDKAALTGAQTEDAEYFCALWNNHVSF 242	Db	258 GGCKLTVLGLEAPAAAAPDSKSDSKAOYSA 288	
Qy	238 GGCKLTVLGQPKSAAAGSEOKLJSEEDLNS 251	RESULT 10	Qy	RESULT 9
Db	243 GGCKLTVLGKRAA 256	ID AAR22582 standard; protein; 256 AA.	Qy	AAR56483 standard; protein; 435 AA.
XX		XX	XX	
AC		AC	AC	
DE		DE	DE	
XX		XX	XX	
DT		DT	DT	
XX		XX	XX	
21-MAY-1992 (first entry)				
ScFvB18 construct mutant #1.				

fragment was cloned into fdDOGkan (fdCAT2 with the tet gene replaced by a kanamycin resistance gene) to give fdDOCKansfB18, or into the phagemid PHEN1 to create PHEN1-scrB18. The constructs were used to test the effect of using mutator strains to increase the diversity of the cloned genes. The strains NR9046 mutD5 : NR9046 mutD5 : Tn10 and NR9046 mutT1 : NR9046 mutT1 : Tn10 were constructed by P1 transduction. After 4 rounds of mutation and screening, 40 phage inserts were sequenced. They each displayed single mutations in 6 different positions, five being in the light chain region. More than 70% of the mutations occurred at positions 724 and 725 (of the nucleotide sequence) changing the first Gly in the J segment (framework 4) to Ser (in 21 cases, as shown here) or Asp (in 3 cases). The mutant fragments had affinities for NP which were comparable to the wild-type scfv fragment (20nM). N.B. fdCAT2 is also referred to as fd-tet-tet-DOG1 and fdDOG1. See also AAR21260-307, 309-311; AAR22450, 565-581

) Sequence 256 AA;

RESULT 15
R22586
AAR22586 standard; protein; 256 AA.

AAR22586;

21-MAY-1992 (first entry)

SfFvB18 construct #5.

Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;
g3P; binding; adsorption; gene VIII; diverse repertoire;
specific binding pairs; replicable genetic disassembly package.

Synthetic. Key Difference 202
Location/Qualifiers
Misc-difference 202
/label = mutation

WO9201047-A.	23-JAN-1992.	10-JUL-1990;	90GB-00015198.
		10-JUL-1990;	90GB-00015198.
		19-OCT-1990;	90GB-00022845.
		12-NOV-1990;	90GB-000224503.
		13-NOV-1990;	90GB-000224503.

PR 06-MAR-1991; 91GB-0004744.
 PR 15-MAY-1991; 91GB-00010549.
 XX
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA (MEDI-) MED RES COUNCIL.
 XX
 PI Mccafferty J, Pope AR, Johnson ES,
 Jackson RH, Holliger KP, Marks JD,
 XX DR WPI: 1992-056662/07.
 DR N-PSDB; AAQ23862.
 XX
 PT Producing members of specific binding pairs - by expression in
 PT recombinant host cells with a secreting replicable genetic display
 package.
 PT

Example 38; Fig 44; 209pp; English.

The sequence is encoded by an antibody scFv fragment directed against 4-hydroxy-3-nitrophenylacetic acid (NP). HV and LV chains of an MAb against NP were separately amplified and reassembled to form the construct, which was then ligated into the fd gene III contig vector, fdCAT2, derived from fdTPS/Xh. (See AAQ21095.) The clone having the scFVB18 sequence fused in frame to gene III was designated fdCAT2scFVB18. Alternatively the fragment was cloned into fdDOCKan (fdCAT2) with the tet gene replaced by a kanamycin resistance gene to give fdDOCKkanscFVB18, or into the phagemid pHEN1 to create pHEN1-scFVB18. The constructs were used to test the effect of using mutator strains to diversify the diversity of the cloned genes. The strains NR904mutD5; NR904mutD5: Tn10 and NR904mutT1; NR904 mutT1: Tn10 were constructed by P1 transduction. After 4 rounds of mutation and screening, 40 phage inserts were sequenced. They each displayed single mutations in 6 different positions, five being in the light chain region. More than 70% of the mutations occurred at positions 724 and 725 (of the nucleotide sequence) changing the first Gly in the J segment (framework 4) to Ser (in 21 cases) or Asp (in 3 cases, as shown here). The mutant fragments had affinities for NP which were comparable to the wild-type scFv fragment (20AM). N.B. fdCAT2 is also referred to as fd-tet-DG1 and fdDOCK1. See also AAR21260-307, 309-311; AAR22450, 565-581.

Query Match	Best Local Similarity	Score	DB	Length
Matches 199; Conservative	78.34%; Pred. No. 2e-61;	68.64%; Score 1008.5;	DB 2;	Length 256;
2 AQQOLQSGAELARPGEASVMSCKSACKASCGTFTTYTIHVQRPGHDLIEWIGYINPSSGYSD	61			
6 AQQOLQSGAELVKGASVKLSCKSACKASCGTFTSYWMMKVKOREPGRGLIEWIGIDPNSCGTTK	65			
62 YNQNFKEGTTLTDKSSNTATMQLNLTSEDSAVYCARRADGNYEYTWFAYWGCGTTV	121			
66 YNEKFPSKSKATLTVKDPSSTATMQLNLTSEDSAVYCA-RDYDGSSYY--PDYGCGTTV	122			
122 TVSS---AKTPKLGGSDIQAIVTGTGSALTSPGETVTLTCRSNTGTVTTSNYANWYQEK	177			
123 TVSSGGCGCGCGCGCGSQAVGTGTOESALTSPGETVTLTCRSNTGAVTTSNYANWYQEK	182			
178 PDLFLFGLIGHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIFYFCALWYNNWVFG	237			
183 PDLFLFGLIGHTNNRAGVPARFSGSLIGDKAALITGAQTEDEAIFYFCALWYSNHWVFD	242			
238 GGTKLTVLGQPKSA	251			
243 GGTKLTVLEIKRA	256			

Search completed: February 9, 2006, 03:27:47
Job time: 283.175 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 9, 2006, 03:28:13 ; Search time 26.5346 Seconds
(without alignments)
989.922 Million cell updates/sec

Title: US-10-049-404-3

Perfect score: 1470

Sequence: 1 MAQVQLQQSGAEELARPGASV.....GSEQLISBEDLNSHHHHH 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext. 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 0%
Listing First 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602.5	41.0	268	A56446	Ig heavy chain V r peB leader/Ig hea
2	578	39.3	287	PC4402	Ig lambda chain V
3	572	38.9	214	PC4406	Ig lambda-1 chain V
4	562	38.2	113	B54256	Ig lambda chain V
5	558	38.0	128	S52450	Ig lambda chain V
6	556	37.8	129	LIMS4E	Ig lambda-1 chain V
7	551.5	37.5	112	S06818	Ig lambda chain V
8	536	36.5	113	S06819	Ig lambda chain V
9	531.5	36.2	249	S41374	single chain Fv
10	528.5	36.0	114	S06822	Ig lambda chain V
11	527.5	35.9	474	G2MS11	Ig gamma-2b chain
12	526	35.8	106	S20654	Ig lambda chain V
13	524.5	35.7	114	S06820	Ig lambda chain V
14	520	35.4	129	L2MS35	Ig lambda-2 chain
15	515	35.0	113	S06821	Ig lambda chain V
16	506.5	34.5	139	PS0024	Ig heavy chain pre
17	502	34.1	99	S14582	Ig lambda chain V
18	493.5	33.6	99	PH1089	Ig lambda chain V
19	493	33.5	140	PH1482	Ig heavy chain V r
20	492	33.5	116	L1MSV	Ig lambda-1 chain
21	492	33.5	119	S20640	Ig heavy chain V r
22	491	33.4	97	PH1090	Ig lambda chain V
23	489	33.3	99	S14584	Ig lambda chain V
24	489	33.3	100	PH1088	Ig lambda chain V
25	482	32.8	246	S38950	Ig gamma chain - m
26	482	32.8	446	S40295	Ig gamma-2a chain
27	481.5	32.8	139	A27609	Ig heavy chain pre
28	481	32.7	117	JC2269	PL7-6 antibody he
29	480.5	32.7	128	C37267	Ig heavy chain V r

RESULT 1

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J.Biol.Chem. 270, 7829-7835, 1995

A:Title A high affinity digoxin-binding protein displayed on M13 is functionally identical

A:Reference number: A56446; PMID: 95229583; PMID: 7713873

A:Accession: A56446

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-268 <TAN>

A:Cross-references: UNIPARC:UPI00001706D0; GB:U20617

C:Keywords: heterotetramer; immunoglobulin

Query Match 41.0%; Score 602.5; DB 2; Length 268;

Best Local Similarity 47.8%; Pred. No. 7.6e-35; Indels 25; Gaps 7;

Matches 133; Conservative 45; Mismatches 75;

Query 1 MAQVLOOQS...GAEELARPAGSVKMSKASGYTFPTTYHVRQRPHDLEWIGYINPSSGYS 60

Db 1 MAQVLOQ...GAEELARPAGSVKMSKASGYTFPTTYHVRQRPHDLEWIGYINPSSGYS 60

Query 1 MAQVLOOQS...GAEELARPAGSVKMSKASGYTFPTTYHVRQRPHDLEWIGYINPSSGYS 60

Db 1 MAQVLOQ...GAEELARPAGSVKMSKASGYTFPTTYHVRQRPHDLEWIGYINPSSGYS 60

Query 61 DYNQNPKGKTTLTDADKSNTAYMQLNLSLTSEDASAVVYCARRADYGVYETTWFA-YWQGQT 119

Db 61 KYDPKFQGRATIAADTSNTAYLQLLSSLTSEDASAVVYCA-----SYYLTRYENWQGQT 114

Query 120 TVTIVSS---AKTPKLGGDIQAVVTVQEA-LTSPGETVTLITRSNTGTVTTSMYANTV 174

Db 115 TVTIVSSGGGGSDGSGGSDTIELOTAISMSLGEKVTMSCRASSV---NFIYWW 170

Query 175 QEKPDHLFTGLIGHTNRNAPGVPARFSGSLIGDAALTTGAOTDEAAYFCALMWNHW 234

Db 171 QKSDASPLKWLWYTFIHLPPGPVAPFSGSGSGNSLTTSSMEGBDAATYCOQTSSPF 230

Query 235 VFGGGTKLTVLGQPKSAA-----AGSEOKLISSEBDLN 266

Db 233 TFGSCTKLEI---KRSAAHHHHGAAEQLISSEBDLN 265

C:Species: Synthetic

C:Date: 06-Nov-1998 #sequence_revision 06-Nov-1998 #text_change 06-Nov-1998

C:Accession: PC4402

R: Suzuki, C.; Ueda, H.; Nagamune, T.

J.Biochem. 122, 322-329, 1997

A:Title Construction, bacterial expression, and characterization of haptenspecific si

A:Reference number: PC4402

A;Accession: PC4402
A;Molecule type: DNA
A;Residues: 1-287 <SU2>
A;Cross-references: UNIPARC:UPI000017CF08
C;Keywords: fusion protein

Query Match 39.3%; Score 578; DB 4; Length 287;
Best Local Similarity 82.2%; Pred. No. 4.1e-33; Indels 0; Gaps 0;
Matches 111; Conservative 7; Mismatches 17;

Qy 130 PKLGGDIAQVVTQESALTTSPGETVTLTCRSNTGTVITTSNYANWQEKPDHLLFTGLIGHT 189
Db 19 PAVAMDIQAVVTQESALTTSPGETVTLTCRSNTGTVITTSNYANWQEKPDHLLFTGLIGHT 78

Qy 190 NNRAPGPVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWFEGGTKLTVLGPK 249
Db 79 NNRAPGPVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWFEGGTKLTVLSSAD 138

Qy 250 SAARGSEKQLISEED 264
Db 139 DARKKDARKDDAKD 153

RESULT 3
PC1156 Ig lambda chain V region MabB23 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
C;Accession: PC4156
R;Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
Gene 169, 237-239, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a monoclonal antibody from a mouse hybridoma cell line. A;Accession number: PC4155; MUID:96194809; PMID:8647454
A;Molecule type: mRNA
A;Cross-references: UNIPARC:UPI0000115C8; GB:U28967; NID:gi1262178; PID: AAC52488.1; PDB: 1P8-110/Region: V region
C;Superfamily: immunoglobulin V region; immunoglobulin homology
P;130-198/Domain: immunoglobulin homology

Query Match 38.9%; Score 572; DB 2; Length 214;
Best Local Similarity 93.9%; Pred. No. 7.7e-33; Indels 0; Gaps 0;
Matches 108; Conservative 3; Mismatches 4;

Qy 137 QAVTQESALTTSPGETVTLTCRSNTGTVITTSNYANWQEKPDHLLFTGLIGHTNRAFGV 196
Db 1 QAVTQESALTTSPGETVTLTCRSNTGAVTTQEKPDHLLFTGLIGGTNNRYGV 60

Qy 197 PARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWFEGGTKLTVLGPKSA 251
Db 61 PARFSGSLIGDKAALITGAQTEDEALYFCALWMSNTHWFEGGTKLTVLGPKSS 115

RESULT 4
B51256 Ig lambda-1 chain V region (hybridoma Se155-4) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: B54256; AA4592
R;Bundle, D.R.; Bichler, E.; Gidney, M.A.; Meidal, M.; Ragauskas, A.; Sigurskjold, B.W.; Biochemistry 33, 5172-5182, 1994
A;Title: Molecular recognition of a *Salmonella* trisaccharide epitope by monoclonal antibody Se155-4
A;Accession number: AA45256; MUID:94227048; PMID:751555
A;Molecule type: protein
A;Residues: 1-113 <BUN>
A;Cross-references: UNIPARC:UPI000017682F
A;Experimental source: Se155-4 hybridoma, BALB/c mouse
A;Note: sequence extracted from NCBI backbone (NCBIT:146746)
A;Note: the Se155-4 hybridoma is specific for the 3,6-dideoxy-D-galactose epitope of the C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin F,15-92/Domain: immunoglobulin homology <IMM>
Query Match 38.2%; Score 562; DB 2; Length 113;
Best Local Similarity 92.9%; Pred. No. 1.8e-32; Indels 0; Gaps 0;
Matches 105; Conservative 4; Mismatches 4;

Qy 137 QAVTQESALTTSPGETVTLTCRSNTGTVITTSNYANWQEKPDHLLFTGLIGHTNRAFGV 196
Db 1 QAVTQESALTTSPGETVTLTCRSNTGTVITTSNYANWQEKPDHLLFTGLIGHTNRAFGV 60

Qy 197 PARFSGSLIGDKAALITGAQTEDAIFCALWYNNHWFEGGTKLTVLGPK 249
Db 61 PARFSGSLIGDKAALITGAQPEDEALYFCALWCNNHWFEGGTKLTVLGPK 113

RESULT 5
S52450 Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52450
R;Berdoz, J.; Kraehenbuhl, J.P.
Submitted to the BMBL Data Library, November 1994
A;Description: Specification amplification by the polymerase chain reaction of rearranged gene
A;Reference number: S52445
A;Accession: S52450
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-128 <BER>
A;Cross-references: UNIPARC:UPI0000114E8F; EMBL:X82687; PID:NID:9673448; EMBL:CAAS0008.1; P
C;Genetics:
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>
C;Keywords: heterotetramer; immunoglobulin homology <IMM>
F;34-111/Domain: immunoglobulin homology

Query Match 38.0%; Score 558; DB 2; Length 128;
Best Local Similarity 93.8%; Pred. No. 4e-32; Indels 0; Gaps 0;
Matches 106; Conservative 2; Mismatches 5;

Qy 133 GGDIQAVTQESALTTSPGETVTLTCRSNTGTVITTSNYANWQEKPDHLLFTGLIGHTNRAFGV 192
Db 16 GAIQAVTQESALTTSPGETVTLTCRSNTGAVTTQEKPDHLLFTGLIGHTNRAFGV 75

Qy 193 APGVPARFSGSLIGDKAALITGAQTEDEALYFCALWYNNHWFEGGTKLTVL 245
Db 76 APGVPARFSGSLIGDKAALITGAQTEDEALYFCALWMSNTHWFEGGTKLTVL 128

RESULT 6
L1MS4E Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43)
C;Species: Mus musculus (house mouse)
C;Accession: B93815; B93775; C93784; C93788; A01995
R;Burstein, Y.; Schechter, I.
Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
A;Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor
A;Reference number: A93815; MUID:77148916; PMID:403522
A;Contents: MOPC 104E
A;Accession: B93815
A;Molecule type: protein
A;Residues: 1-29 <BUR>
A;Cross-references: UNIPROT:P01724; UNIPARC:UPI0000173721
A;Note: this precursor was synthesized in a cell-free system directed by messenger RNA
R;Appella, E.
Proc. Natl. Acad. Sci. U.S.A. 68, 590-594, 1971
A;Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
A;Reference number: A93775; MUID:71107854; PMID:5276767
A;Contents: MOPC 104E; RPC 20
A;Accession: B93775

A;Molecule type: protein
A;Residues: 'Z', '21-25, 'Q', '27-129 <APP>
A;Cross-references: UNIPARC:UPI00000173722
A;Accession: C93775
A;Molecule type: protein
A;Residues: 20-129 <AP2>
A;Cross-references: UNIPARC:UPI0000173722
A;Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
R;Cesari, T.M.; Weigert, M.
Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
A;Title: Mouse lambda chain sequences.
A;Reference number: A93784; MUID:90229669; PMID:4516208
A;Contents: J558; S104; S178
A;Molecule type: protein
A;Residues: 20-129 <CES>
A;Cross-references: UNIPARC:UPI0000173723
A;Accession: B93784
A;Molecule type: protein
A;Residues: 20-129 <CE2>
A;Cross-references: UNIPARC:UPI0000173723
A;Accession: C93784
A;Molecule type: protein
A;Residues: 'N', '45-70 'N', '72-115 'R', '117-129 <CB3>
A;Cross-references: UNIPARC:UPI0000173723
A;Note: these proteins were isolated from serum or urine of tumor-bearing mice
R;Bernard, O.; Hozumi, N.; Tonegawa, S.
Cell 15, 1133-1144, 1978
A;Title: Sequences of mouse immunoglobulin light chain genes before and after somatic ch
A;Reference number: A90780; MUID:79084170; PMID:103630
A;Contents: H2020
A;Accession: A90780
A;Molecule type: DNA
A;Residues: 'I'-43, 'T', '45-50, 'G', '52-58, 'E', '60-89, 'D', '91-129 <BER>
A;Cross-references: UNIPARC:UPI0000027085
A;Note: the sequence was determined from the differentiated gene
R;Bothwell, A.L.M.; Paskind, M.; Reth, M.; Imanishi-Kari, T.; Rajewsky, K.; Baltimore, D
Nature 298, 380-382, 1982
A;Title: Somatic variants of murine immunoglobulin lambda light chains.
A;Reference number: A93282; MUID:82220143; PMID:6283385
A;Contents: S43
A;Accession: C93282
A;Molecule type: DNA
A;Residues: 'E', '60-89, 'D', '91-98, 'T', '100-105, 'M', '107-129 <BOT>
A;Cross-references: UNIPARC:UPI0000027087
A;Note: the sequence was determined from the differentiated gene
C;Comment: The MOPC 104E sequence is shown.
A;Introns: 16/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κ) ap
band disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; pyroglutamic acid
F;1-19/Domain: Signal sequence #status experimental <SIG>
F;20-129/Domain: Ig λ-domain chain precursor V region #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IMM>
F;20/Modified site: Pyrrolidine carboxylic acid (Gln) (in mature form) #status experiment
F;41-109/Disulfide bonds: #status predicted

Query Match Score 556; DB 1; Length 129;
Best Local Similarity 92.1%; Pred. No. 5.6e-32;
Matches 105; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

RESULT 9
S41374 single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Accession: S41374
R;Arteenco, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
Submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antib
A;Reference number: S41374

S06818
Ig lambda chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: S06818
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mo
A;Reference number: S06815; MUID:9064531; PMID:2555519
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-112 <ML>
A;Cross-references: UNIPARC:UPI000017683F
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F; 15-92/Domain: immunoglobulin homology <IMM>
Query Match Score 551.5%; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 9.8e-32;
Matches 105; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
Qy 138 AVVTOESA-LTTSGETVTLCRSNTGTIVTISNYANWQEKPDHLFTGLIGHTNNRAPGV 196
Db 1 AVVTOESAXLTTSGETVTLCRSSTGAVTTSNYANWQEKPDHLFTGLIGHTNNRAPGV 60
Qy 197 PARFGSLIGDKAAALITGAQTEDAIYFCALWVNNHWFEGGTKLTVLGQP 248
Db 61 PARFGSLIGDKAAALITGAQTEDAIYFCALWTSNHWVFFGGTKLTVLGQP 112
RESULT 8
S06819
Ig lambda chain V region (clone 10C3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
C;Accession: S06819
R;Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mo
A;Reference number: S06815; MUID:9064531; PMID:2555519
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-113 <ML>
A;Cross-references: UNIPARC:UPI000011583C; EMBL:X17168; PIDN:952251; PMID:2555519
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin F; 14-91/Domain: immunoglobulin homology <IMM>
F;21-89/Disulfide bonds: #status predicted

Query Match Score 536; DB 2; Length 113;
Best Local Similarity 94.4%; Pred. No. 1.2e-30;
Matches 102; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 138 AVVTOESALTTSGETVTLCRSNTGTIVTISNYANWQEKPDHLFTGLIGHTNNRAPGV 197
Db 1 AVVTOESALTTSGETVTLCRSSTGAVTTSNYANWQEKPDHLFTGLIGHTNNRAPGV 60
Qy 198 ARFGSLIGDKAAALITGAQTEDAIYFCALWVNNHWFEGGTKLTVLG 245
Db 61 ARFGSLIGDKAAALITGAQTEDAIYFCALWTSNHWVFFGGTKLTVLG 108
RESULT 9
S41374 single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Accession: S41374
R;Arteenco, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
Submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antib
A;Reference number: S41374

Db 19 SEVQLQQSGPDELUNPGASVRMSCKASGGTFTITYMMWVKQPGQGLEWIGYINPNKDDGK 78
 Qy 62 YNQNFKGKTTLTADKSSNTAYMOLNSLTSSEDAVYYCARRADYGNEXTYTFAYWGGGTV 121
 :|:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 79 FNEKFRGKATLTDKSSNTAYMELSSLTSSEDAVYYCARR-----dydxwfatwggtlv 133
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Mar-1980 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
 C;Accession: A93431; B93282; B91462; A99410; S09331; A01997
 R;Rn, G.; Govindji, N.; Horzumi, N.; Murialdo, H.
 Nucleic Acids Res 10, 3831-3843, 1982
 A;Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene
 A;Reference number: A93431; MUID:82274221; PMID:6287422
 A;Accession: A93431
 A;Molecule type: mRNA
 A;Residues: 1-129 <WUG>
 A;Cross-references: UNIPROT:P01739; UNIPARC:UPI00000270BD
 R;Bothwell, A.L.M.; Parkind, M.; Reth, M.; Imanishi Kari, T.; Rajewsky, K.; Baltimore,
 Nature 298, 380-384, 1982
 A;Title: Somatic variants of murine immunoglobulin lambda light chains.
 A;Reference number: A93282; MUID:82220143; PMID:6283385
 A;Accession: B93282
 A;Molecule type: DNA
 A;Residues: 1-129 <BOT>
 A;Cross-references: UNIPARC:UPI00000270BD
 A;Note: the sequence was determined from the differentiated gene
 R;Schechter, I.; Wolf, O.; Zamelli, R.; Burstein, Y.
 Fed. Proc. 38, 1839-1845, 1979
 A;Title: Structure and function of immunoglobulin genes and precursors.
 A;Reference number: A91462; MUID:79148758; PMID:428562
 A;Accession: B91462
 A;Molecule type: protein
 A;Residues: 1-122 <SCH>
 A;Cross-references: UNIPARC:UPI0000173724
 R;Dugan, E.S.; Bradshaw, R.A.; Simms, E.S.; Eisen, H.N.
 Biochemistry 12, 5400-5416, 1973
 A;Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).
 A;Reference number: A90372; MUID:74048693; PMID:4760498
 A;Accession: A90372
 A;Molecule type: protein
 A;Residues: 20-24, 'E', 'D', 'D', 'D', 75-129 <DUG>
 A;Cross-references: UNIPARC:UPI0000173725
 R;Gavish, M.; Zukut, R.; Wilchek, M.; Givol, D.
 Biochemistry 17, 1345-1351, 1978
 A;Title: Preparation of a semisynthetic antibody
 A;Reference number: A90410; MUID:7818754; PMID:18802
 A;Accession: A90410
 A;Molecule type: protein
 A;Residues: 1-129 <GAV>
 A;Cross-references: UNIPARC:UPI00000270BD
 R;Bogen, B.; Lambiris, J.D.
 EMBO J. 8, 1947-1952, 1989
 A;Title: Minimum length of an idiotypic peptide and a model for its binding to a major
 A;Reference number: S09391; MUID:90053397; PMID:2792076
 A;Accession: S09391
 A;Molecule type: protein
 A;Residues: 110-126 BOG>
 A;Cross-references: UNIPARC:UPI0000173726
 C;Comment: This chain is from a myeloma protein with anti-DNP activity.
 C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (K₁)
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; pyrogulamic acid
 F;1-19/Domain: signal sequence #status experimenter <SIG>
 F;20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>
 F;34-111/Domain: immunoglobulin homology <IMM>
 F;110-126/Region: idiotype to histocompatibility complex class II #status experimental
 F;20/Modified site: Pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
 F;41-109/Disulfide bonds: #status predicted
 Query Match 35.7% Score 524.5; DB 2; Length 114;
 Best Local Similarity 93.6%; Pred. No. 7.4e-30;
 Matches 102; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 C;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mouse
 A;Accession: S06820
 A;Molecule type: mRNA
 A;Residues 1-14 <WIL>
 A;Cross-references: UNIPARC:UPI0000176812; EMBL:X17169
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;15-92/Domain: immunoglobulin homology <IMM>
 F;22-90/Disulfide bonds: #status predicted
 Query Match 35.7% Score 524.5; DB 2; Length 114;
 Best Local Similarity 93.6%; Pred. No. 7.4e-30;
 Matches 102; Conservative 2; Mismatches 4; Indels 1; Gaps 1;
 C;Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mouse
 A;Accession: S06820
 A;Molecule type: mRNA
 A;Residues 1-14 <WIL>
 A;Cross-references: UNIPARC:UPI0000176812; EMBL:X17169
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F;15-92/Domain: immunoglobulin homology <IMM>
 F;22-90/Disulfide bonds: #status predicted
 Query Match 35.4% Score 520; DB 1; Length 129;
 Best Local Similarity 85.1%; Pred. No. 1.8e-29;
 Matches 97; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 133 GGDIOAVVTOESALTTSPETVTILCRSMNTGTVTTSNANWQEKPDILFTGLIGHTNNR 192
 Db 16 GASSQAVVTOESALTTSPETVTILCRSMNTGTVTTSNANWQEKPDILFTGLIGTSNR 75

Qy 193 APGVPARFSGSLICGDKAALTITGAOTEDAIFYCALWNNHWFGGGTKLTVLG 246
 Db 76 APGVPVRLFSGSLICGDKAALTITGAOTEDDAMYCALWPRNHFVGGGTKVTVLG 129

RESULT 15

S06821
 Ig lambda chain V region (clone 11C7) - mouse
 CSpecies: Mus musculus (house mouse)
 CDate: 30-Jun-1992 #sequence_revision 11-Nov-1994 #text_change 21-Jan-2000
 CAccesion: S06821
 R.Miller III, A.; Glassel, J.A.
J. Mol. Biol. 209, 763-778, 1989
 A.Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-mo^r
 A.Reference number: S06815; MUID:90064531; PMID:2555519
 A.Accession: S06821
 A.Molecule type: mRNA
 A.Residues: 1-113 <MIL>
 A.Cross references: UNIPARC:UPI0000115E3E; EMBL:X17170; NID:9522253; PID:CAA35048.1; P10
 A.Notes: the authors translated the codon AGT for residue 47 as Gly, GTT for residue 56 a
 C.Superfamily: immunoglobulin V region; immunoglobulin homology
 C.Keywords: heterotetramer; immunoglobulin
 F:14-91/Domain: immunoglobulin homology <IMM>
 P:21-89/Disulfide bonds: #status predicted

Query Match 35.0%; Score 515; DB 2; Length 113;
 Best Local Similarity 86.6%; Pred. No. 3.e-29;
 Matches 97; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 138 AVTQESALTTSPETVTILCRSMNTGTVTTSNANWQEKPDILFTGLIGHTNNRACPVP 197
 Db 1 AVTQESLTTSPETVTILCRSMNTGTVTTSNANWQEKPDILFTGLIGHTNNRACPVP 60

Qy 198 ARFGSLICGDKAALTITGAOTEDAIFYCALWNNHWFGGGTKLTVLGQPK 249
 Db 61 ARFGSLICGDKVALTIGQTEDAIYCALWISNHLVGGGTRLVQPE 112

Search completed: February 9, 2006, 03:34:19
 Job time : 27.5346 secs

GenCore version 5.1.7
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Om protein - protein search, using sw model
Run on: February 9, 2006, 03:18:36 ; Search time 167.882 Seconds
(without alignments)
1147.288 Million cell update/sec

Title: US-10-049-404-3
Perfect score: 1470
Sequence: 1 MAQVQLQSGAELARPGASV.....GSEQRKLISEEDLNHHHHH 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 0%
Listing first 45 summaries

Database : UniProt_05_80_*
1: uniprot_sprot:
2: uniprot_trembl:
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	597	40.6	243	Q7TQM2_MOUSE
2	590	40.1	487	Q65ZL2_HUMAN
3	559	38.0	129	I1V1D_MOUSE
4	557	37.9	129	I1V1B_MOUSE
5	556	37.8	129	I1V1B_MOUSE
6	555	37.8	110	I1V1C_MOUSE
7	548.5	37.3	113	QBCGS1_MOUSE
8	545	37.1	129	QBVDDE2_MOUSE
9	539	36.7	225	QKBK05_MOUSE
10	538.5	36.6	109	Q9BT13_MOUSE
11	533	36.3	244	O65ZC8_HUMAN
12	520	35.4	129	I1V2B_MOUSE
13	519.5	35.3	473	O3D8L4_MOUSE
14	512.5	34.9	617	O4KML5_MOUSE
15	510	34.7	241	Q92IA6_MOUSE
16	499	33.9	468	Q569W9_MOUSE
17	494.5	33.6	117	I1V1A_MOUSE
18	490	33.3	120	I1V03_MOUSE
19	487	33.1	220	Q65ZC9_HUMAN
20	481	32.7	472	QEPJA7_MOUSE
21	480	32.7	140	I1V02_MOUSE
22	479.5	32.6	463	Q9BL4C_MOUSE
23	479	32.6	616	O504M7_MOUSE
24	478.5	32.6	465	Q6BJB2_MOUSE
25	476	32.4	470	Q7TMK1_MOUSE
26	472	32.1	168	Q8VDC9_MOUSE
27	472	32.1	458	Q5BjZ2_rat
28	469.5	31.9	613	Q8VCX7_MOUSE
29	468.5	31.9	489	Q8VCX4_MOUSE
30	466.5	31.7	139	I1V01_MOUSE
31	466	31.7	Q65ZR6_MOUSE	

ALIGNMENTS

RESULT 1		Q7TQM2_MOUSE PRELIMINARY;		PRT; 243 AA.	
ID	Q7TQM2	Q7TQM2	MOUSE	PRELIMINARY;	
AC	Q7TQM2	Q7TQM2			
DT	01-OCT-2003	(TREMBLrel.	25,	Created)	
DT	01-OCT-2003	(TREMBLrel.	25,	Last sequence update)	
DT	01-MAR-2004	(TREMBLrel.	26,	Last annotation update)	
DE	ScFv 6H8 Protein (Fragment)				
GN	Name=scFv 6H8				
OS	Mus musculus				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murine; Mus.				
OX	NCBI TaxID:10090;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=Balb/C;				
RX	Medline=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;				
RA	Peter J.C., Ettekhari P., Billiard P., Wallukat G., Roebke J.; "scFv single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor."				
RT	J. Biol. Chem. 278:36740-36747 (2003).				
RL	DR				
DR	AJ574851; CAB00495.1.; Genomic_DNA.				
DR	HSSP_P01751; 1A6N.				
DR	InterPro_IPR007110; Ig-like.				
DR	InterPro_IPR003596; Ig_v.				
DR	SMART_SM00406; Ig_v.				
DR	PROSITE_PSS0335; Ig_LIKE.				
FT	NON_TER_1				
SQ	SEQUENCE 243 AA; 25976 MW; BEFFF64D2DCP4F76 CRC64;				
Query Match	40.6%	Score 597; DB 2;	Length 243;		
Best Local Similarity	47.3%	Pred. No. 2.6-39;			
Matches 131;	Conservative 23;	Mismatches -77;	Indels 40;	Gaps 6;	
Qy	3 QVQLQSGAELARPGASVNSCKAGCTTFTYIHWYRQPHDLEWIGYINPSSGYSYD 62				
Db	1 QVQLQSGSELVPGASVLSCKASCYTFTYIHWYRQPHDLEWIGYINPSSGYSYD 60				
Qy	63 NQNFKGKTTLTAQKSNTATMOLNSLTSEDAVYICARRADYGYNTBYTFWYQGQTIVT 122				
Db	61 DEFKNGKGILTVDTSSSTAHMHSLLASESAVYICARGG --- RGLDWGAGTTLT 113				
Qy	123 VSSAKTPKLGG-----DIQAVTQESALITSPGTIVTLCRSGNTGTVTISNYANWVQE 176				
Db	114 VSSGGGSGGGGGSDIQ-MTQSSSFVSLGRVTTKASDIY--NRLAQYQQ 169				
Qy	177 KPDHLPTGLIGHTNNRAGPAPFSGLIGDKALTITGAQTEDAIYCALWYNHWVF 236				
Db	27 472 32.1 168 2 Q8VDC9_MOUSE				
Qy	28 469.5 31.9 613 2 Q8VCX7_MOUSE				
Db	29 468.5 31.9 489 2 Q8VCX4_MOUSE				
Qy	30 466.5 31.7 139 1 I1V01_MOUSE				
Db	31 466 31.7 Q65ZR6_MOUSE				

CC use as long as its content is in no way modified and this statement is not removed.

CC HSSP; P01724; IgV.
DR P01727; 20-129.
DR Ensembl; ENSMUSG0000064012; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003396; Ig_v.
DR PROSITE; PS50835; Ig_LIKE; 1.
KW Immunoglobulin domain; Immunoglobulin V region; Signal.

FT SIGNAL 1 19
CHAIN 20 129 Ig lambda-1 chain V region S43.
FT DOMAIN 20 125 Ig-like.
FT NON_TER 129 129
SQ SEQUENCE 129 AA: 13529 MW: 84E54ETDD5791345 CRC64;

Query Match 37.9% Score 557; DB 1; Length 129;
Best Local Similarity 90.1%; Pred. No. 1.8e-36;
Matches 105; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 133 GGDIOAVTQVTOESALTSPSEPTVLTCRSNTGTTTSNTANWQEKPDHLPTGLIGHTNRR 192
Db 16 GAISSQAVTVQESALTSPSEPTVLTCRSNTGATTTSNTANWQEKPDHLPTGLIGTNRR 75

Qy 193 APGVPARFSSGLIDPKAALITGAQTEDAIYFCALWNHNVGGGFLTVLG 246
Db 76 APGVPARFSSGLIDPKAALITGAQTEDAMYFCALWNHNVGGGFLTVLG 129

RESULT 5

LV1B_MOUSE STANDARD; PRT; 129 AA.
AC P01724;
DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
IG lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
NCB_TaxID=10090;

RN PROTEIN SEQUENCE OF 1-29 (MOPC 104E), AND SEQUENCE REVISION TO 20 AND
RP 26.
RX MEDLINE=77148916; PubMed=43522;

RA Burstein Y.; Schechter I.;
RT "Amino acid sequence of the NH2-terminal extra piece segments of the
precursors of mouse immunoglobulin lambda-type and kappa-type light
chains.";
RT Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).

[2] RN PROTEIN SEQUENCE OF 20-129 (MOPC 104E AND RPC 20).
RX MEDLINE=71107854; PubMed=5276767;

RA Appella E.;
RT "Amino acid sequences of two mouse immunoglobulin lambda chains.";
RT Proc. Natl. Acad. Sci. U.S.A. 68:530-534(1971).

[3] RN PROTEIN SEQUENCE OF 20-129 (J558 AND S104).
RX MEDLINE=73229659; PubMed=4516208;

RA Cesari I.M.; Weigert M.;
RT "Mouse lambda-chain sequences";
Proc. Natl. Acad. Sci. U.S.A. 70:2112-2116(1973).
RL "Mouse lambda-chain sequences";
CC -!- MISCELLANEOUS: Compositions and partial sequences of RPC 20 show
no differences from MOPC 104E. The sequences of J558 and S104
seems identical with that shown.
CC -!- MISCELLANEOUS: These proteins were isolated from serum or urine of
tumor-bearing mice.
CC -!- MISCELLANEOUS: The MOPC 104E precursor was synthesized in a cell-
free system directed by mRNA isolated from MOPC 104E myeloma
polysomes. Met-1 was lacking in 90% of the chains. It is probably
rapidly cleaved after synthesis.

-!- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC DR PIR: B33815; LIMS4E.
DR PDB: 1A6U; X-ray; L=21-128.
DR PDB: 1A6V; X-ray; L/M/N=20-128.
DR PDB: 1A6W; X-ray; L=21-128.
DR Ensembl: ENSEMBL00000064012; Mus musculus.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003516; Ig_v.
DR SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
KW 3D-structure; Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrrolidone carboxylic acid; Signal.
FT SIGNAL 1 19
FT CHAIN 20 129 Ig lambda-1 chain V regions MOPC
FT FT DOMAIN 20 125 Ig-like.
FT FT MOD_RES 20 20
FT FT NON_TER 129 129
FT FT STRAND 23 25
FT FT TURN 28 31
FT FT STRAND 33 34
FT FT TURN 36 43
FT FT STRAND 44 45
FT FT SPAND 46 46
FT FT HELIX 50 52
FT FT STRAND 55 60
FT FT TURN 61 63
FT FT STRAND 64 64
FT FT TURN 71 73
FT FT STRAND 74 75
FT FT TURN 77 78
FT FT TURN 81 82
FT FT STRAND 83 88
FT FT TURN 89 90
FT FT STRAND 91 97
FT FT HELIX 101 103
FT FT STRAND 105 112
FT FT STRAND 117 119
FT FT STRAND 123 127
SQ SEQUENCE 129 AA; 13479 MW; 03629939D5791AC0 CRC64;
Query Match 37.8% Score 556; DB 1; Length 129;
Best Local Similarity 92.1%; Pred. No. 2.1e-36;
Matches 105; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 133 GGDIOAVTQVTOESALTSPSEPTVLTCRSNTGTTTSNTANWQEKPDHLPTGLIGHTNRR 192
Db 16 GAISSQAVTVQESALTSPSEPTVLTCRSNTGATTTSNTANWQEKPDHLPTGLIGTNRR 75
Qy 193 APGVPARFSSGLIDPKAALITGAQTEDAIYFCALWNHNVGGGFLTVLG 246
Db 76 APGVPARFSSGLIDPKAALITGAQTEDAMYFCALWNHNVGGGFLTVLG 129

RESULT 6

LV1C_MOUSE STANDARD; PRT; 110 AA.
ID LV1C_MOUSE
AC P01725;
DT 21-JUL-1986 (Rel. 01; Created)
DT 21-JUL-1986 (Rel. 01; Last sequence update)
DT 10-MAY-2005 (Rel. 47; Last annotation update)
DB IG lambda-1 chain V region S178.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Muridae; Murinae; Mus.
OC Murioidea; Muridae; Murinae; Mus.

DE	ScFv B8E5 protein (Fragment).
GN	Name=CFCV B8E5;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
NCBI_TaxID	10090;
[1]	RN
	NUCLEOTIDE SEQUENCE.
RC	STRAN=BalB/c;
RA	Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
RA	Briand J.P., Hoebeka J.,
RA	"Modulation of the M2 muscarinic acetylcholine receptor activity with monoclonal anti-M2 receptor antibody fragments.",
RT	J. Biol. Chem. 279: 55597-55706 (2004)
RT	EMBL: AJ746180; CAG34081.1; -; Other_DNA.
DR	HSSP: P01837; 1KCR.
DR	InterPro: IPR003599; 19.
DR	InterPro: IPR07110; 19-like.
DR	InterPro: IPR03396; 19_v.
DR	SMART: SM00409; IG; 2.
DR	SMART: SM00406; IgV; 2.
DR	PROSITE: PSS0835; IG_LIKE; 2.
DN	NON_TER_1
FT	SEQUENCE 255 AA:
SQ	2445 MW; B68BD38395DF713B CRC64;
	Query Match 36.7%; Score 539; DB 2; Length 255;
	Best Local Similarity 41.3%; Pred. No. 1.1e-34;
	Matches 116; Conservative 39; Mismatches 90; Indels 36; Gaps 6
Qy	3 QVQLQSGAELARPGASVMSCKASGYFTTYIIVRQPGRHDLIEWIGYINPSSGYSVD 62
Db	1 QVQLQSGAELARPGASVMSCKASGYFTTYIIVRQPGRHDLIEWIGYINPSSGYSVD 60
Qy	63 NONFKGKTTLADKSNTAYMQLNSLTSEDSAVYCARRADYGNEYTW.FAYWGGTV 121
Db	61 PDSTYGRFTPSDQNAKTLYLQMSLKSDEAMYCARHI--NRYDGAFDYWGQGTTL 117
Qy	122 TVVSSAKTTPKLGG-----DIQAVVYTOESALTTSPGETVTTLTCRSMNTGTVTT--SNYAN 172
Db	118 TVVSSGGGGCGGGGGCGGGSDI-YMAQSPSSLSVAEGKVMSCKSQSLNSRNQNYLA 176
Qy	173 WVQBPKDHLPTGLIGHTNNRAGPVAFRSGLIGKAALTGTGAQTEDEATYFCALWYNN 232
Db	177 WYQQPGQSPKLIVYGAStRESGVDPRTGSQGSCDTFLTIISSVQDAFLVYQNDHSY 236
Qy	233 HWVFGGGTKLTIVLGQPKSAAGSEQKLISEEDLNSHHHHH 273
Db	237 PLTFAGTKLEI-----KHHHHHH 255
	RESULT 1.0
OBT13	MOUSE PRELIMINARY;
ID	Q8ET13_MOUSE PRELIMINARY;
AC	Q8ET13_;
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Immunoglobulin light chain variable region (Fragment).
OS	Mus musculus (Mouse)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC	Muridae; Murinae; Mus.
NCBI_TaxID	10090;
[1]	RN
	NUCLEOTIDE SEQUENCE.
RC	STRAN=BalB/c;
RA	Song M.-Y., Kang H.-K., Kwag W.-J., Moon H.-J., Song T.-H., Ko I.-Y.;
RL	Submitted (JUL-2000) to the ENB/GenBank/DBJ databases.
DR	EMBL: AF287275; AAGG03033.1; -; mRNAs.
DR	HSSP: P01724; 1A6V.
SMR	Q8ET13; 1A6V.
DR	Ensembl: ENSMUSG00000064012; Mus musculus.

Db	19	SVQLQSGAELAKPGASVQLCKSKASAGTFSYWMHWVKQRFGQLEWIGYNPSSGTYK	78	
Db	62	YNNQFKGKTTLADKSNTAYMOLNSLTSESDAVYCARRADGYNEYTWFAWYGOSTV	121	
Db	79	YQKFQKATLADKSNTAYMOLNSLTSESDAVYCARRADGYNEYTWFAWYGOSTV	137	
Db	122	TYS -AKTPKLGGDIQAVVTTQESALITSPGETVTLTCRSNTGTVTISNYAWQEKPDH	180	
Db	138	TVSSESQSFPP ---NVFPLVSCESPL ---SDKNLVAMGCTARDFLPSTISF-TWNYQNNTTE	190	
Db	181	LFTGLIGHTNNAPIGPVPARFSGSLIGDIAAATGAAQFEDAYIFCALWYNNHWFEGGT	240	
Db	191	VIQGIRTFPTLRTGKYLATSQWLSPKSIL---EGSDDEVL-VCKTHY-----GGKN	238	
Db	241	K-----LTVLGOPK---SAAGSBEKLISE	262	
Db	239	KDLHVPIPAVAMNPVNVPVRDGFSGPAPRSKLICE	278	
RESULT 15				
	Q921A6_MOUSE			
	ID Q921A6_MOUSE PRELIMINARY;	PRT;	241 AA.	
	AC Q921A6;			
	DT 01-DEC-2001 (TREMBLrel. 19, Created)			
	DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
	DT 01-MAR-2004 (TREMBLrel. 20, Last annotation update)			
	DE Anti -CEA 79 single chain Fv (Fragment).			
	OS Mus musculus (Mouse)			
	Mammalia; Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus .			
	OC NCBI - Taxid=10090;			
	RN [1]			
	RP NUCLEOTIDE SEQUENCE.			
	RX MBDLINB=98170165; PubMed=9509426;			
	RX MEDLINE=9134142L; RX			
	RA Chung J.H., Choi S.J., Kim H.J., Choi I.H., Lee S.D.,			
	RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K., Chung H.K.,			
	RT "Cloning and characterization of cDNAs encoding VH and VL of a monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain Fv molecule (scFv).";			
	RT Mol. Cells 7:816-819(1997).			
	RL [2]			
	RP NUCLEOTIDE SEQUENCE.			
	RX MEDLINE=9134142L; RX			
	RA Stark S.E., Caton A.J.;			
	RT "Antibodies that are specific for a single amino acid interchange in a protein epitope use structurally distinct variable regions.";			
	RT J. Exp. Med. 174:613-624(1991).			
	DR EMBL; U88057; AAB48044.1; - ; mRNA.			
	DR PIR; S19965; S19965.			
	DR PIR; S19967; S19967.			
	DR PIR; S19968; S19968.			
	DR PIR; S26325; S26325.			
	DR HSSP; P01607; 18MW.			
	DR Ensembl; ENSMUS00000021155; Mus musculus.			
	DR Interpro; IPR00110; 19-like.			
	DR Interpro; IPR003596; 19_v.			
	DR SMART; SM00406; IgV_2.			
	DR PROSITE; PS50835; Ig_LIKE; 2.			
	FT NON_TER 1_1			
	FT NON_TER 241_241			
	SQ SEQUENCE 241 AA;	26086 MW;	027688724889C771 CRC64;	
Query Match	34.7%	Score 510;	DB 2;	Length 241;
Best Local Similarity	44.1%	Pred. No. 2.1e-32;		
Matches	113	Conservative 43; Mismatches 64; Indels 36; Gaps 9;		
Qy	3	QVQLOQSSAELARP GASVYMSCKASAGTFTTIHWQRPHDLEWIGYINPSSGKSDY	62	
Db	1	QVKLQSSPPELLKPKGETVKKSKASAGTFTIDGMNWYKQAPGKGLKMGWINTGPEYI	60	
Qy	63	NONFKGKTTTADKSNTAYMOLNSLTSESDAVYCARRADGYNEYTWFAWYGOSTV	122	

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 9, 2006, 03:33:41 ; Search time 36.2299 Seconds
 (without alignments)
 622.979 Million cell updates/sec

Title: US-10-049-404-3
 Perfect score: 1470
 Sequence: 1 MAQVOLQQSAGELAQLRPGASV.....GSEQLISEEDLNHHHHH 273

Scoring table: BLOSUM62
 Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgns2_6/podata/1/iaa/5_COMB.pep.*
 2: /cgns2_6/podata/1/iaa/6_COMB.pep.*
 3: /cgns2_6/podata/1/iaa/H_COMB.pep.*
 4: /cgns2_6/podata/1/iaa/FETUS_COMB.pep.*
 5: /cgns2_6/podata/1/iaa/RE_COMB.pep.*
 6: /cgns2_6/podata/1/iaa/backfilles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	103.5	70.6	1	03-08-491-988-9	Sequence 9, Appli	
2	103.5	70.4	402	1	US-08-491-988-7	Sequence 7, Appli
3	103.5	70.4	435	1	US-08-491-988-5	Sequence 5, Appli
4	102.6	67.5	1	US-08-491-988-1/2	Sequence 72, Appli	
5	102.6	69.8	269	1	US-08-491-988-3	Sequence 3, Appli
6	73.0	49.7	288	2	US-09-423-439-38	Sequence 38, Appli
7	69.6	47.3	495	2	US-09-423-004-18	Sequence 2, Appli
8	68.5	46.6	258	2	US-09-526-738A-4	Sequence 4, Appli
9	67.8	46.1	239	2	US-08-279-772A-8	Sequence 8, Appli
10	67.8	46.1	239	1	US-08-902-886-11	Sequence 11, Appli
11	67.7	46.1	246	1	US-08-469-886-57	Sequence 57, Appli
12	67.7	46.1	246	1	US-08-469-658-57	Sequence 57, Appli
13	67.6	46.0	256	2	US-09-126-738A-2	Sequence 2, Appli
14	67.5	45.9	599	1	US-08-463-163-3	Sequence 3, Appli
15	65.9	44.9	244	1	US-08-553-497A-20	Sequence 20, Appli
16	65.7	44.7	273	1	US-08-033-853-18	Sequence 18, Appli
17	65.4	44.5	246	1	US-08-553-497A-24	Sequence 24, Appli
18	65.0	44.3	673	2	US-09-423-439-32	Sequence 32, Appli
19	64.8	44.1	270	2	US-09-76-118-2	Sequence 2, Appli
20	64.5	43.8	264	2	US-10-114-716A-46	Sequence 46, Appli
21	64.1	43.6	244	1	US-08-553-497A-22	Sequence 22, Appli
22	63.4	43.1	267	2	US-09-119-788-30	Sequence 30, Appli
23	63.4	43.1	553	1	US-08-661-052-16	Sequence 16, Appli
24	63.4	43.1	553	2	US-09-188-082-16	Sequence 16, Appli
25	63.4	43.1	553	2	US-09-364-088-16	Sequence 16, Appli
26	63.4	43.1	553	2	US-09-102-716-16	Sequence 16, Appli
27	63.1	43.0	242	1	US-08-553-497A-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1
 US-08-491-988-9
 ; Sequence 9, Application US/08491988
 ; Patent No. 5973116
 ; GENERAL INFORMATION:
 ; APPLICANT: OPENETOS, AGAMEMNON A.
 ; ATTORNEY/AGENT INFORMATION:
 ; APPLICANT: SPOONER, ROBERT A.
 ; ATTORNEY: DEONARAIN, MAHENDRA
 ; TITLE OF INVENTION: Compounds for targeting
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: MCALAY NISSEN GOLDBERG KIEL & HAND, LLP
 ; STREET: 261 MADISON AVENUE
 ; CITY: NEW YORK
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10016-2391
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/491_988
 ; FILING DATE: 18-DEC-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GOLDBERG, JULBS E.
 ; REGISTRATION NUMBER: 24_408
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-818-9479
 ; TELEFAX: 212-818-9479
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-491-988-9
 ; Query Match 70.6%; Score 1037.5%; DB 1; Length 402;
 ; Best Local Similarity 78.1%; Pred. No. 4_6e-70;
 ; Matches 203; Conservative 17; Mismatches 33; Indels 7; Gaps 2;

Qy 1 MAQVOLQQSAGELAQLRPGASV.....GSEQLISEEDLNHHHHH 60
 Db 21 MAQVOLQQSAGELAQLRPGASV.....GSEQLISEEDLNHHHHH 80
 Qy 61 DYNQNPFKGKHTLADKSNTAYMQNLSLTSEDSAVYCARRADIGNYETWFAWCQGTT 120

Page 2

RESULT 2
US-08-491-988-7

Sequence 7, Application US/08491988
Patent No. 5973116.

GENERAL INFORMATION:

APPLICANT: EPIENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA

TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESS: MCALUAY NISSSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-5

Query Match 70.4%; Score 1035.5; DB 1; Length 435;
Best Local Similarity 74.9%; Pred. No. 6.7e-10;
Matches 203; Conservative 22; Mismatches 39; Indels 7; Gaps 2;

Qy 1 MAQVQLQSGAELARPGASVKNMSCKASCGYTFTYTHWQRPGDLEWIGIGYINPSSEYS 60
Db 21 MAQVQLQGPGLVKGASVKLSCKASGYFTSYMMWKGRLPGRGLEWIGRIDPNSGT 80

Qy 61 DYNQNFKGKTTLTADKSNTAYMQLNSLTSEDSAVYCARRADYGNYETMFAYNGQGT 120
Db 81 KYNKEFKSKATLTVDKSSTAMQSLSTSEDSAVYCAR--YDYGSSYFDWQGQTT 137

Qy 1 MAQVQLQSGAELARPGASVKNMSCKASCGYTFTYTHWQRPGDLEWIGIGYINPSSEYS 60
Db 21 MAQVQLQGPGLVKGASVKLSCKASGYFTSYMMWKGRLPGRGLEWIGRIDPNSGT 80

Qy 61 DYNQNFKGKTTLTADKSNTAYMQLNSLTSEDSAVYCARRADYGNYETMFAYNGQGT 120
Db 81 KYNKEFKSKATLTVDKSSTAMQSLSTSEDSAVYCAR--YDYGSSYFDWQGQTT 137

Qy 121 VTVSS---AKTPKLGGDIQAVVTOESALTSPGETVTLTCRSNTGTTTSNYANWQE 176
Db 138 VTVSSCGGGCGGGCGGSQAVVTSPGETVTLTCRSSTGAVTTSNYANWQE 197

Qy 121 VTVSS---AKTPKLGGDIQAVVTOESALTSPGETVTLTCRSNTGTTTSNYANWQE 176
Db 138 VTVSSCGGGCGGGCGGSQAVVTSPGETVTLTCRSSTGAVTTSNYANWQE 197

RESULT 3
US-08-491-988-5

Sequence 5, Application US/08491988
Patent No. 5973116.

GENERAL INFORMATION:
APPLICANT: EPIENETOS, AGAMEMNON A.
APPLICANT: SPOONER, ROBERT A.
APPLICANT: DEONARAIN, MAHENDRA

TITLE OF INVENTION: Compounds for targeting
NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:
ADDRESS: MCALUAY NISSSEN GOLDBERG KIEL & HAND, LLP
STREET: 261 MADISON AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/491,988
FILING DATE: 18-DEC-1995
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: GOLDBERG, JULES E.
REGISTRATION NUMBER: 24,408
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-986-4090
TELEFAX: 212-818-9479
INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 435 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-491-988-5

Query Match 70.4%; Score 1035.5; DB 1; Length 435;
Best Local Similarity 74.9%; Pred. No. 7.1e-70;
Matches 203; Conservative 22; Mismatches 39; Indels 7; Gaps 2;

Qy 1 MAQVQLQSGAELARPGASVKNMSCKASCGYTFTYTHWQRPGDLEWIGIGYINPSSEYS 60
Db 21 MAQVQLQGPGLVKGASVKLSCKASGYFTSYMMWKGRLPGRGLEWIGRIDPNSGT 80

Qy 61 DYNQNFKGKTTLTADKSNTAYMQLNSLTSEDSAVYCARRADYGNYETMFAYNGQGT 120
Db 81 KYNKEFKSKATLTVDKSSTAMQSLSTSEDSAVYCAR--YDYGSSYFDWQGQTT 137

Qy 121 VTVSS---AKTPKLGGDIQAVVTOESALTSPGETVTLTCRSNTGTTTSNYANWQE 176
Db 138 VTVSSCGGGCGGGCGGSQAVVTSPGETVTLTCRSSTGAVTTSNYANWQE 197

Qy 121 VTVSS---AKTPKLGGDIQAVVTOESALTSPGETVTLTCRSNTGTTTSNYANWQE 176
Db 138 VTVSSCGGGCGGGCGGSQAVVTSPGETVTLTCRSSTGAVTTSNYANWQE 197

RESULT 4

ZIP: 10016-2391
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/491,988
 FILING DATE: 18-DEC-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: GOLDBERG, JULES E.
 REGISTRATION NUMBER: 24,108
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 112-986-4900
 TELEFAX: 212-818-9419
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 269 amino acids
 TYPE: amino acid
 TOPology: linear
 MOLECULE TYPE: protein
 US-08-491,988-3

	Query Match	Score: 69.8%	Length: 106.5;	DB 1;	Length: 269;	
Qy	MAQVQLQQSGAELARPGASVYKMSCKASGYFTFTYTHMYRQRPHDLEWIGYINPSSGYS	60				
Db	MAQVQLQQSGAELARPGASVYKMSCKASGYFTFTYTHMYRQRPHDLEWIGYINPSSGYS	60				
Qy	DYNQNFKGTTLTAQKSNTAMQLNLSITSEDAVYYCARRADYGNEYETWRAYGOGTT	120				
Db	DYNQNFKGTTLTAQKSNTAMQLNLSITSEDAVYYCARRADYGNEYETWRAYGOGTT	120				
Qy	KYNEEFKSKATLTVKPSSTAYMQLSITSEDAVYYCARRADYGNEYETWRAYGOGTT	137				
Db	KYNEEFKSKATLTVKPSSTAYMQLSITSEDAVYYCARRADYGNEYETWRAYGOGTT	137				
Qy	ATTPPTPLGGDIAQVWVQESALTTSPETVLTCRENTTGTIVTSNANWQE	176				
Db	ATTPPTPLGGDIAQVWVQESALTTSPETVLTCRENTTGTIVTSNANWQE	176				
Qy	KPDHILFTGLIGHTNRAPGVPARFGSLIGDKAALTITGAQTEDAIYFCALWYTNHWVF	236				
Db	KPDHILFTGLIGHTNRAPGVPARFGSLIGDKAALTITGAQTEDAIYFCALWYTNHWVF	236				
Qy	GGGTLVVLG 246					
Db	GGGTLVVLG 267					

RESULT 6
 US-09-423-439-38
 Sequence 38, Application US/09423439
 ; Patent No. 6339070
 ; GENERAL INFORMATION:
 ; APPLICANT: EMERY, Stephen Charles
 ; BLAKEY, David Charles
 ; TITLE OF INVENTION: CHEMICAL COMPOUNDS
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Winthrop, L.L.P.
 ; STREET: 1100 New York Ave., N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/423,439
 ; FILING DATE: 09-No. 6339070-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06363/002001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 542 5070
 TELEFAX: 617 542 8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 246 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-486-57

Query Match 46.1%; Score 677; DB 1; Length 246;
 Best Local Similarity 55.1%; Pred. No. 2,76-43;
 Matches 146; Conservative 29; Mismatches 70; Indels 20; Gaps 6;

Qy 3 QVQLQQSAELARPGASVMSCKASGYTFTTYHWVRQPHDLEWGYINPSSGYSYD 62
 Db 1 QVKLQQSAELVKGGASVMSCKASGYTFTASYWINWVTKRPGGLEWGHIVPVSITKY 60

Qy 63 NONFKGKTTLADKSSNTAYMQLNSLTSRDAVYCCARRADGNETWFAYGQGTIVT 122
 Db 61 NEKEPKSATLTLDTSSSTAYMQLSLSLTDSSSTAYMQLSLSLTDSSSTAYMQLSLSL 117

Qy 123 VSSAKTTPKLGGD1QAVVTOQESA_LTTSGETUTLTCSNTGTVTTSYANWQEKPDHL 181
 Db 118 VSSG----GGCSDIELTQSPATLSSAGGKVMTCAASSV---SYMHWYQQKCGSS 167

Qy 182 FTGLIGHTNNRAPGVPARFGSLIGDKAALITTAQTEATYFCALWYNHWFGGCTK 241
 Db 168 PKPWIYATSNLASGVPTRSGTSGTSSLTISERVEADATYCOQMSRNPTFGGCTK 227

Qy 242 LTVLGQPKSAAAGSEQKLISEEDLN 266
 Db 228 LEI----KRAAA--EQKLISEEDLN 246

RESULT 12
 US-08-469-658-57
 Sequence 57, Application US/08469658
 Patent No. 5917018

GENERAL INFORMATION:
 APPLICANT: Th egersen, Hans Christian
 APPLICANT: Holtet, Thor Las
 APPLICANT: Etzeoldt, Michael
 TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF PROTEINS
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02110-2804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,658
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/192,060
 FILING DATE: February 4, 1994

CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06363/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 542 5070
 TELEFAX: 617 542 8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 246 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-658-57

Query Match 46.1%; Score 677; DB 1; Length 246;
 Best Local Similarity 55.1%; Pred. No. 2,76-43;
 Matches 146; Conservative 29; Mismatches 70; Indels 20; Gaps 6;

Qy 3 QVQLQQSAELARPGASVMSCKASGYTFTTYHWVRQPHDLEWGYINPSSGYSYD 62
 Db 1 QVKLQQSAELVKGGASVMSCKASGYTFTASYWINWVTKRPGGLEWGHIVPVSITKY 60

Qy 63 NONFKGKTTLADKSSNTAYMQLNSLTSRDAVYCCARRADGNETWFAYGQGTIVT 122
 Db 61 NEKEPKSATLTLDTSSSTAYMQLSLSLTDSSSTAYMQLSLSLTDSSSTAYMQLSLSL 117

Qy 123 VSSAKTTPKLGGD1QAVVTOQESA_LTTSGETUTLTCSNTGTVTTSYANWQEKPDHL 181
 Db 118 VSSG----GGCSDIELTQSPATLSSAGGKVMTCAASSV---SYMHWYQQKCGSS 167

Qy 182 FTGLIGHTNNRAPGVPARFGSLIGDKAALITTAQTEATYFCALWYNHWFGGCTK 241
 Db 168 PKPWIYATSNLASGVPTRSGTSGTSSLTISERVEADATYCOQMSRNPTFGGCTK 227

Qy 242 LTVLGQPKSAAAGSEQKLISEEDLN 266
 Db 228 LEI----KRAAA--EQKLISEEDLN 246

RESULT 13
 US-09-526-738A-2
 Sequence 2, Application US/09526738A
 Patent No. 6630584

GENERAL INFORMATION:
 APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH & INDUSTRIAL DEVELOPMENT LTD.
 APPLICANT: LTD.
 TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
 FILE REFERENCE: 1196336
 CURRENT APPLICATION NUMBER: US/09/526,738A
 CURRENT FILING DATE: 2000-03-16
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 2
 LENGTH: 256
 TYPE: PRT
 ORGANISM: Humanus
 US-09-526-738A-2

Query Match 46.0%; Score 676; DB 2; Length 256;
 Best Local Similarity 55.8%; Pred. No. 3,36-43;
 Matches 145; Conservative 32; Mismatches 59; Indels 24; Gaps 6;

Qy 3 QVQLQQSAELARPGASVMSCKASGYTFTTYHWVRQPHDLEWGYINPSSGYSYD 62
 Db 1 QVKLQQSAELVKGGASVMSCKASGYTFTASYWINWVTKRPGGLEWGHIVPVSITKY 60

Qy 63 NONFKGKTTLADKSSNTAYMQLNSLTSRDAVYCCARRADGNETWFAYGQGTIVT 122
 Db 61 NQKFQDKATLAAKSSTAYMQLSLSLNDSAVYCTT-----GYSYFDWQGQTIVT 113

Query 123 VSSAKTTPKLGG-----DIQAVVYQESA-LITSPGETVTLTCRSNTGTVTTSNYANVQ 175
 Database 114 VSSGGGGGGGGGGGGSD-E--LIQSPAIMSAFGKERVITCASSSVY---NYMHTFQ 167
 Query 176 EKDPLHFTGLIGHTNRAPIGVPARFSGSLJGDKAALTITGACTEDEAAYFCALWNNHW 235
 Database 168 QKEPRTSPKLWISSTSNLASCYPARFSGSGTSLTSLRMEADAATYCQORSSYPT 227
 Query 236 FGGGTRKLTULQGPNSAAAGS 255
 Database 228 FGGGTRKL---QIKRAAGA 243

RESULT 14
 US-08-46-163-3
 Sequence 3, Application US/08463163
 Patent No. 5696237

GENERAL INFORMATION:

APPLICANT: FitzGeneral, David J.
 APPLICANT: Chaudhary, Vijay K.
 APPLICANT: Pastan, Ira H.
 APPLICANT: Waldmann, Thomas A.
 APPLICANT: Queen, Cary L.

TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Townsend and Townsend and Crew
 STREET: One Market Plaza, Steuart Street Tower
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94105-1492

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,163
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 536

PRIOR APPLICATION DATA:

FILING DATE: 22-JAN-1981
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/227,227
 FILING DATE: 24-SEP-1986
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/341,361
 FILING DATE: 21-APR-1989
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/865,722
 FILING DATE: 08-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen L.
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 015280-12211
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 543-9600
 TELEFAX: (415) 543-5043
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 599 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-463-163-3

Query Match 45.9%; Score 675; DB 1; Length 599;
 Best Local Similarity 53.9%; Pred. No. 1.1e-42;
 Matches 146; Conservative 31; Mismatches 78; Indels 16; Gaps 4;

Query 3 QVQLOQSGAELARGASVYRMSCKASGYTFETTYTHWVORPGHDEWIGYINPSGSYSDY 62
 Database 2 QVQLOQSGAELARGASVYRMSCKASGYTFETTYTHWVORPGHDEWIGYINPSGSYDYE 61
 Query 63 NQNFKGKTTLTADKSNTAYMQLNLSITSDSAYTCARRADGYEYTTFAYNGQGTTV 122
 Database 62 NQKFKDALKLTADKSSTAYMQLNLSITFDSAYTCARCGV-----FDYNGQGTTL 114
 Query 123 VSS---AKTPKGKGGDIOAVVTSBAA-LITTSPEBTVLTCRSNTGTVTTSNYANWQEK 177
 Database 115 VSSGGGGGGGGGGGGGGGGSOIVLTQSPAIMSASPEKVUTITCSAS---SSISYHWFQOK 170
 Query 178 PDHMLFTGLIGHTNRAPIGVPARFSGSLIGDKAALTITGAQTEDAIYPICALWNNHWVFG 237
 Database 171 PGTSPLKWLXTTNSIASGYPARFSGSSETSYTSIRNMEAEDATYCHQRTSTYPLTFG 230
 Database 238 GGTLTULQGPNSAAAGSOKLISEEDLNH 268
 Database 231 SGTKLELKGGSLAALTQACHLPLETFTRH 261

RESULT 15
 US-08-55-497-A-20
 Sequence 20, Application US/08553497A
 Patent No. 5844093

GENERAL INFORMATION:

APPLICANT: KETTLEBOROUGH, C. A.
 APPLICANT: BENDIG, MARY M.
 APPLICANT: ANSELL, KEITH H.
 APPLICANT: GUSSON, DETLEF
 APPLICANT: ADAN, JAUME
 APPLICANT: MITJANS, FRANCESCA
 APPLICANT: ROSELL, ELSABET
 APPLICANT: BIASCO, FRANCESC
 APPLICANT: PIULATS, JAUME
 TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MILLIEN, WHITE, ZELIANO & BRANTGAN, P.C.
 STREET: 2200 CLARENDON BLVD. SUITE 1400
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: US
 ZIP: 22201
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/553,497A
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/EP95/00978
 FILING DATE: 16-MAR-1995
 PRIORITY INFORMATION:
 PRIORITY NUMBER: EP 08/553,497A
 FILING DATE: 17-NOV-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/EP95/00978
 FILING DATE: 16-MAR-1995
 PRIORITY NUMBER: EP 94104160.0
 FILING DATE: 17-MAR-1994
 PRIORITY NUMBER: EP 94118970.6
 FILING DATE: 02-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: HAMLET-KING, DIANA
 REGISTRATION NUMBER: 33,302
 REFERENCE/DOCKET NUMBER: MERCK 1726
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-243-6333
 TELEFAX: 703-243-6410
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 244 amino acids

;	TYPE:	amino acid
;	TOPOLOGY:	linear
;	MOLECULE TYPE:	protein
US-08-553-497A-20		
Query Match	44.9%	Score 659.5; DB 1; Length 244;
Best Local Similarity	55.8%	Pred. No. 5.4e-42;
Matches 140;	Conservative 33;	Mismatches 61; Indels 17; Gaps 7;
Qy	3	QVQLQSGAELARPGASVYKMSCKASGTVFTPTTYTHAWRQRPHDLEWICYINPSSGYSDY 62
Db	1	EVLQQLQSGAELVKGASVRLSKCAGSITFTSHMWHWRAGQCLEWGBFTNSNGRNY 60
Qy	63	NQNPKGKTTLADKSNTAYMQLNLSSEDSAVYYCARADGMYEYTWFAYNGQGTIVT 122
Db	61	NEKPKSKATLTYDKSSSTAYMQLNLSSEDSAVYYCASR-DY-DYDGRYFDYNGQGTIVT 118
Qy	123	VSSARTTPKLG-----DIAQVTPQSA-LITSPGEVTLLTRCSNTGTVTTSYANWQ 175
Db	119	VSSGGGGGGGGGGSDIE--ITQSPAIMSASPGEKVTMTCSASSSV---SYMMYQ 172
Qy	176	EKDPLHIFTGLIGHTNRAAPGVPARFSGSLIGDKAALITGAAQTEDAYIFCALW-YNNH 233
Db	173	QRPGSPPRLIYDTNSLNLASGPVYRFSGSGSGTSYSTLTISRMEADEAATYCCQWSVSYPPM 232
Qy	234	WVEGGGSKKLTV 244
Db	233	YTFGGGSKKLTVDEI 243

Search completed: February 9, 2006, 03:35:35
Job time : 37,2299 secs

Result No.	Score	Query Match	Length DB	ID	Description
1	709	48.2	492	4	US-10-682-845-81
2	707	48.1	492	4	US-10-682-845-81
3	707	48.1	492	4	US-10-682-845-81
4	706	48.1	492	4	US-10-682-845-81
5	706	48.0	492	4	US-10-682-845-81
6	705	48.0	492	4	US-10-682-845-81
7	704	47.9	409	4	US-10-362-521-2
8	704	47.9	492	4	US-10-682-845-81
9	704	47.9	492	4	US-10-682-845-81
10	704	47.9	492	4	US-10-682-845-81
11	704	47.9	500	4	US-10-168-809-22
12	703	47.8	492	4	US-10-682-845-83
13	702	47.8	492	4	US-10-682-845-67
14	701	47.7	492	4	US-10-682-845-65
15	701	47.7	492	4	US-10-682-845-75
16	700.5	47.7	243	5	US-10-179-934-10
17	700.5	47.7	243	5	US-10-610-432-10
18	700	47.6	295	4	US-10-406-830-7
19	700	47.6	492	4	US-10-682-845-77
20	699	47.6	492	4	US-10-682-845-69
21	696	47.3	495	3	US-10-948-904-18
22	696	47.3	495	5	US-10-672-932-18
23	686	46.7	260	4	US-10-435-614-20
24	685	46.6	258	4	US-10-247-488-4
25	684	46.5	260	4	US-10-135-614-19
26	683.5	46.5	249	3	US-09-080-748-1838
27	683.5	46.5	249	4	US-10-293-418-1838

US-10-682-845-63
; Sequence 63, Application US/10682845
; Publication No. US2004016241A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIORITY FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 63
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M4 mutant in anti-CD3 part
US-10-682-845-63

Query Match 48.1%; Score 707; DB 4; Length 492;
Best Local Similarity 51.6%; Pred. No. 1.le-41;
Matches 148; Conservative 30; Mismatches 57; Indels 52; Gaps 7;

Qy 2 AQVLOQSGAELLARPASVMSKASGVTFTTYIHWVRQPHDLEIIGYINPSSGYSD 61
Db 243 SDIKLQQSGAELLARPASVMSKCTSGTPTRYMHWKQRPGGLEIIGYINPSRGYTN 302

Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAYYCARRADGNYEYTWFAYWGOQTTV 121
Db 303 YNQKFKDATLTDKSSSTAYMOLSSLTSEDSAYYCARYND---EHYCLDYWQGQTL 358

Qy 122 TVSSAKTPKLGG-----DIQAVVYQESA-LTTSPEGETLTLCRSNTGVT 166
Db 359 TVSSVE----GCGGGSGGGSGVDDQ--LTQSPAIMSASPGEKVTMTCRASSV-- 409

Qy 167 TSYANWVQKPDHLFTGLIGHTNRAFGVPARSGSLGKALITGAQTEDEAIVFC 226
Db 410 -SYMANWVQKSGSTSPKRWYDTSKVASGVYPRFGSGSGTSYSLTISMEAEDATTYC 467

Qy 227 ALWYNNHNVFGGTKLTVLGQPKSAAGSEQKLISEEDLNHHHHH 273
Db 468 QQNSSNPLTFGAGTKLEL-----KHHHHHH 492

RESULT 4
US-10-682-845-85
; Sequence 85, Application US/10682845
; Publication No. US2004016241A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 85
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M69 mutant in anti-CD3 part
US-10-682-845-85

Query Match 48.1%; Score 707; DB 4; Length 492;
Best Local Similarity 51.9%; Pred. No. 1.le-41;
Matches 149; Conservative 28; Mismatches 58; Indels 52; Gaps 7;

Qy 2 AQVLOQSGAELLARPASVMSKASGVTFTTYIHWVRQPHDLEIIGYINPSSGYSD 61
Db 243 SDIKLQQSGAELLARPASVMSKCTSGTPTRYMHWKQRPGGLEIIGYINPSRGYTN 302

Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAYYCARRADGNYEYTWFAYWGOQTTV 121
Db 303 YNQKFKDATLTDKSSSTAYMOLSSLTSEDSAYYCARYND---EHYCLDYWQGQTL 358

Qy 122 TVSSAKTPKLGG-----DIQAVVYQESA-LTTSPEGETLTLCRSNTGVT 166
Db 359 TVSSVE----GCGGGSGGGSGVDDQ--LTQSPAIMSASPGEKVTMTCRASSV-- 409

Qy 167 TSYANWVQKPDHLFTGLIGHTNRAFGVPARSGSLGKALITGAQTEDEAIVFC 226
Db 410 -SYMANWVQKSGSTSPKRWYDTSKVASGVYPRFGSGSGTSYSLTISMEAEDATTYC 467

Qy 227 ALWYNNHNVFGGTKLTVLGQPKSAAGSEQKLISEEDLNHHHHH 273
Db 468 QQNSSNPLTFGAGTKLEL-----KHHHHHH 492

RESULT 3
US-10-682-845-73
; Sequence 73, Application US/10682845
; Publication No. US2004016241A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2296 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 73
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M13 mutant in anti-CD3 part
US-10-682-845-73

Query Match 48.1%; Score 707; DB 4; Length 492;

RESULT 5
US-10-682-845-61
Sequence 61; Application US/10682845
Publication No. US2004016241A1
GENERAL INFORMATION:
TITLE OF INVENTION: Potent T cell modulating molecules
FILE REFERENCE: G2296 US
CURRENT APPLICATION NUMBER: US/10/682,845
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: US 60/419,149
PRIOR FILING DATE: 2002-10-18
PRIOR APPLICATION NUMBER: CA 2,403,313
PRIOR FILING DATE: 2002-10-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 61
LENGTH: 492
TYPE: PRT
FEATURE: artificial sequence
OTHER INFORMATION: scFv EpcamXCD3 with M1 mutant in anti-CD3 part
US-10-682-845-61

Query Match 48.0%; Score 706; DB 4; Length 492;
Best Local Similarity 51.6%; Pred. No. 1.3e-41;
Matches 148; Conservative 29; Mismatches 58; Indels 52; Gaps 7;

Qy 2 AQVQLOQSGAELARGASVKSCKASGYTFTTYTHWQRPHDLEWIGYINPSSGSD 61
Db 243 SDIKLQQSGAELARGASVKSCKTSCTGIFTYTMHWVRQPGLEWIGYINPSRGYTN 302

Qy 62 YNQNFKGKTTLADKSNTAYMQLNSLTSEDSAYYCARRADGYNEYTWFAWGOQTV 121
Db 303 YNQKEFDKATLTOKSSSTAYMQLNSLTSEDSAYYCARRYHID---DHYCLDWGQGTTL 358

Qy 122 TVSSAKTPKLGG-----DIQAVVTOESA-LTTSPGETVTLTCRSNTGTVT 166
Db 359 TVSSV-----GGSGSGSGGGSGGGYDDIQ---LTTSPAIMSASGEKVTMTCRASSV-- 409

Qy 167 TSNYANWQEKPDHLFTGLIGHTNNRAGVPARFGSLIGDKAALITGAOTDEAIYFC 226
Db 410 --SYNNWYQOKSGTSKPKRWIYDTSKVAGSVPYRFSGSGTSYLTISMEAADATYTC 467

Qy 227 ALWYNHHWVGGGTPLKLTGQPKSAAGSFQKLISBEDLNSHHHHH 273
Db 468 QWQSSNPPLTFGAGTKLEL-----KHHHHHH 492

RESULT 7
US-10-362-591-2
Sequence 2; Application US/1062591
Publication No. US20040072749A1
GENERAL INFORMATION:
APPLICANT: ZOCHER, MARCEL,
APPLICANT: BAERLE, PATRICK
APPLICANT: DREIER, TORSTEN
TITLE OF INVENTION: COMPOSITION FOR THE ELIMINATION OF AUTOACTIVE B-CELLS
FILE REFERENCE: 029976-0110
CURRENT APPLICATION NUMBER: US/10/362,591
CURRENT FILING DATE: 2003-07-21
PRIOR APPLICATION NUMBER: PCT/EP01/09714
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 2
LENGTH: 409
TYPE: PRT
ORGANISM: Homo sapiens
US-10-362-591-2

Query Match 47.9%; Score 704; DB 4; Length 409;
Best Local Similarity 51.6%; Pred. No. 1.5e-41;
Matches 148; Conservative 29; Mismatches 58; Indels 52; Gaps 7;

Qy 2 AQVQLOQSGAELARGASVKSCKASGYTFTTYTHWQRPHDLEWIGYINPSSGSD 61
Db 160 SDIKLQQSGAELARGASVKSCKTSCTGIFTYTMHWVRQPGLEWIGYINPSRGYTN 219

Qy 62 YNQNFKGKTTLADKSNTAYMQLNSLTSEDSAYYCARRADGYNEYTWFAWGOQTV 121
Db 220 YNQKEFDKATLTOKSSSTAYMQLNSLTSEDSAYYCARRYHID---DHYCLDWGQGTTL 275

Qy 122 TVSSAKTPKLGG-----DIQAVVTOESA-LTTSPGETVTLTCRSNTGTVT 166
Db 276 TVSSV-----GGSGSGSGGGSGGGYDDIQ---LTTSPAIMSASGEKVTMTCRASSV-- 326

Qy 167 TSNYANWQEKPDHLFTGLIGHTNNRAGVPARFGSLIGDKAALITGAOTDEAIYFC 226
Db 327 --SYNNWYQOKSGTSKPKRWIYDTSKVAGSVPYRFSGSGTSYLTISMEAADATYTC 384

Qy 227 ALWYNHHWVGGGTPLKLTGQPKSAAGSFQKLISBEDLNSHHHHH 273
Db 385 QWQSSNPPLTFGAGTKLEL-----KHHHHHH 409

RESULT 8
US-10-682-845-59
; Sequence 59, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2/96 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 59
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 (modified antiCD3 VH-region derived from OKT-3)
US-10-682-845-59

Query Match 47.9%; Score 704; DB 4; Length 492;
Best Local Similarity 51.6%; Pred. No. 1.8e-41;
Matches 29; Mismatches 58; Indels 52; Gaps 7;
RESULT 10
US-10-682-845-87
; Sequence 87, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2/96 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 87
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M76 mutant in anti-CD3 part
US-10-682-845-87

Query Match 47.9%; Score 704; DB 4; Length 492;
Best Local Similarity 52.3%; Pred. No. 1.8e-41;
Matches 150; Conservative 27; Mismatches 58; Indels 52; Gaps 8;
; Sequence 75, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2/216 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 75
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M14 mutant in anti-CD3 part
US-10-682-845-75

Query Match 47.9%; Score 704; DB 4; Length 492;
Best Local Similarity 52.3%; Pred. No. 1.8e-41;
Matches 150; Conservative 27; Mismatches 58; Indels 52; Gaps 8;
; Sequence 75, Application US/10682845
; Publication No. US20040162411A1
; GENERAL INFORMATION:
; APPLICANT: Lanzavecchia, Antonio
; TITLE OF INVENTION: Potent T cell modulating molecules
; FILE REFERENCE: G2/216 US
; CURRENT APPLICATION NUMBER: US/10/682,845
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US 60/419,149
; PRIOR FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: CA 2,403,313
; PRIOR FILING DATE: 2002-10-11
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 75
; LENGTH: 492
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: scFv EpCAMxCD3 with M14 mutant in anti-CD3 part
US-10-682-845-75

RESULT 11
 US-10-168-809-22
 Sequence 22, Application US/101688809
 GENERAL INFORMATION:
 APPLICANT: Muller-Hermelink, Hans Konrad
 APPLICANT: GREINER, AXEL
 APPLICANT: DORKEN, BERND
 APPLICANT: BARGOU, RALF
 APPLICANT: KUFER, PETER
 TITLE OF INVENTION: ANTIBODIES AGAINST PLASMA CELLS
 FILE REFERENCE: 009848-0272298
 CURRENT APPLICATION NUMBER: US/10/168, 809
 CURRENT FILING DATE: 2002-06-21
 PRIOR APPLICATION NUMBER: PCT/EP00/13238
 PRIOR FILING DATE: 1999-12-23
 PRIOR FILING DATE: 1999-12-23
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 22
 LENGTH: 500
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: synthetic hybrid, no
 OTHER INFORMATION: Description of Artificial Sequence: synthetic hybrid, no
 OTHER INFORMATION: natural origin
 US-10-168-809-22

Query Match 47.9%; Score 704; DB 4; Length 500;
 Best Local Similarity 51.6%; Pred. No. 1.8e-4;
 Matches 148; Conservative 29; Mismatches 58; Indels 52; Gaps 7;

Qy 2 AQVQLOQGAELARPAGASVMSCKASGYTFTTYTHWQRPGHDLEWIGYINPSSGYS 61
 Db 251 SDIKLQOQGAELARPAGASVMSCKTSGTFTRYTMHWYKQRPGGLEWIGYINPSRGYT 308
 Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTV 121
 Db 311 YNQKFKDATLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTL 356
 Qy 122 TVSSAKTTPKLGG-----DIQAVVTOESA-LTTSPEGETTLTCRSNTGVT 166
 Db 367 TVSSVB----GSGGSGSGGGSGGGVDDIQ--LTQSPAIMSASPGEKVTMTCRASSV-- 417
 Qy 167 TSNYANWVQEKPDKHFLTGLIGHTNNRAGVPAFSGSLLGDRALHTTGAQTEDEAIYFC 226
 Db 418 :-----SYMMWVQKSGTSPKRWYDTSKVASCVPRFGSGSGTSYSLTISMEAADATYC 475
 Qy 227 ALWYNNHNVFGCGSKTKLTVLGPQPKSAAGSEQKLISEEDLNHHHHH 273
 Db 476 QWNSNPPLTFGACTKLEL-----KHHHHHH 500

RESULT 12
 US-10-168-8045-83
 Sequence 83, Application US/10682845
 GENERAL INFORMATION:
 APPLICANT: Lanzavecchia, Antonio
 TITLE OF INVENTION: Potent T cell modulating molecules
 FILE REFERENCE: G2296 US
 CURRENT APPLICATION NUMBER: US/10/682, 845
 CURRENT FILING DATE: 2003-10-10
 PRIOR APPLICATION NUMBER: US 60/419, 149
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: CA 2, 403, 313
 PRIOR FILING DATE: 2002-10-11
 NUMBER OF SEQ ID NOS: 89
 SOFTWARE: PatentIn Version 3.1
 SEQ ID NO: 67
 LENGTH: 492
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: synthetic hybrid, no
 OTHER INFORMATION: scFv EpCAMxCD3 with M9 mutant in anti-CD3 part
 US-10-682-845-67

Query Match 47.8%; Score 702; DB 4; Length 492;
 Best Local Similarity 51.9%; Pred. No. 2.5e-4;
 Matches 149; Conservative 29; Mismatches 57; Indels 52; Gaps 6;

Qy 2 AQVQLOQGAELARPAGASVMSCKASGYTFTTYTHWQRPGHDLEWIGYINPSSGYS 61
 Db 243 SDIKLQOQGAELARPAGASVMSCKTSGTFTRYTMHWYKQRPGGLEWIGYINPSRGYT 308
 Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTV 121
 Db 303 YNQKFKDATLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTL 356
 Qy 122 TVSSAKTTPKLGG-----DIQAVVTOESA-LTTSPEGETTLTCRSNTGVT 166
 Db 359 TVSSVB----GSGGSGSGGGSGGGVDDIQ--LTQSPAIMSASPGEKVTMTCRASSV-- 405
 Qy 167 TSNYANWVQEKPDKHFLTGLIGHTNNRAGVPAFSGSLLGDRALHTTGAQTEDEAIYFC 226
 Db 418 :-----SYMMWVQKSGTSPKRWYDTSKVASCVPRFGSGSGTSYSLTISMEAADATYC 475
 Qy 227 ALWYNNHNVFGCGSKTKLTVLGPQPKSAAGSEQKLISEEDLNHHHHH 273
 Db 476 QWNSNPPLTFGACTKLEL-----KHHHHHH 500

RESULT 13
 US-10-682-845-67

Query Match 47.8%; Score 702; DB 4; Length 492;
 Best Local Similarity 51.9%; Pred. No. 2.5e-4;
 Matches 149; Conservative 29; Mismatches 57; Indels 52; Gaps 6;

Qy 2 AQVQLOQGAELARPAGASVMSCKASGYTFTTYTHWQRPGHDLEWIGYINPSSGYS 61
 Db 243 SDIKLQOQGAELARPAGASVMSCKTSGTFTRYTMHWYKQRPGGLEWIGYINPSRGYT 308
 Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTV 121
 Db 311 YNQKFKDATLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTL 356
 Qy 122 TVSSAKTTPKLGG-----DIQAVVTOESA-LTTSPEGETTLTCRSNTGVT 166
 Db 367 TVSSVB----GSGGSGSGGGSGGGVDDIQ--LTQSPAIMSASPGEKVTMTCRASSV-- 417
 Qy 167 TSNYANWVQEKPDKHFLTGLIGHTNNRAGVPAFSGSLLGDRALHTTGAQTEDEAIYFC 226
 Db 418 :-----SYMMWVQKSGTSPKRWYDTSKVASCVPRFGSGSGTSYSLTISMEAADATYC 475
 Qy 227 ALWYNNHNVFGCGSKTKLTVLGPQPKSAAGSEQKLISEEDLNHHHHH 273
 Db 476 QWNSNPPLTFGACTKLEL-----KHHHHHH 500

RESULT 14
 US-10-682-845-83
 Sequence 83, Application US/10682845
 GENERAL INFORMATION:
 APPLICANT: Lanzavecchia, Antonio
 TITLE OF INVENTION: Potent T cell modulating molecules
 FILE REFERENCE: G2296 US
 CURRENT APPLICATION NUMBER: US/10/682, 845
 CURRENT FILING DATE: 2003-10-10
 PRIOR APPLICATION NUMBER: US 60/419, 149
 PRIOR FILING DATE: 2002-10-18
 PRIOR APPLICATION NUMBER: CA 2, 403, 313
 PRIOR FILING DATE: 2002-10-11
 NUMBER OF SEQ ID NOS: 89
 SOFTWARE: PatentIn Version 3.1
 SEQ ID NO: 83
 LENGTH: 492
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence: synthetic hybrid, no
 OTHER INFORMATION: scFv EpCAMxCD3 with M9 mutant in anti-CD3 part
 US-10-682-845-67

Query Match 47.8%; Score 702; DB 4; Length 492;
 Best Local Similarity 51.9%; Pred. No. 2.5e-4;
 Matches 149; Conservative 29; Mismatches 57; Indels 52; Gaps 6;

Qy 2 AQVQLOQGAELARPAGASVMSCKASGYTFTTYTHWQRPGHDLEWIGYINPSSGYS 61
 Db 243 SDIKLQOQGAELARPAGASVMSCKTSGTFTRYTMHWYKQRPGGLEWIGYINPSRGYT 308
 Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTV 121
 Db 303 YNQKFKDATLTADKSNTAYMOLNSLTSEDSAYYCARRADYGNEYTWFAVYWGQTTL 356
 Qy 122 TVSSAKTTPKLGG-----DIQAVVTOESA-LTTSPEGETTLTCRSNTGVT 166
 Db 359 TVSSVB----GSGGSGSGGGSGGGVDDIQ--LTQSPAIMSASPGEKVTMTCRASSV-- 405
 Qy 167 TSNYANWVQEKPDKHFLTGLIGHTNNRAGVPAFSGSLLGDRALHTTGAQTEDEAIYFC 226
 Db 418 :-----SYMMWVQKSGTSPKRWYDTSKVASCVPRFGSGSGTSYSLTISMEAADATYC 475
 Qy 227 ALWYNNHNVFGCGSKTKLTVLGPQPKSAAGSEQKLISEEDLNHHHHH 273
 Db 476 QWNSNPPLTFGACTKLEL-----KHHHHHH 500

RESULT 14
 US-10-682-845-65
 ; Sequence 65, Application US/10682845
 ; Publication No. US2004016241A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lanaveccchia, Antonio
 ; TITLE OF INVENTION: Potent T cell modulating molecules
 ; FILE REFERENCE: G2246 US
 ; CURRENT APPLICATION NUMBER: US/10/682,845
 ; CURRENT FILING DATE: 2003-10-10
 ; PRIOR APPLICATION NUMBER: US 60/419,149
 ; PRIOR FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: CA 2,403,313
 ; PRIOR FILING DATE: 2002-10-11
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 65
 ; LENGTH: 492
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: scFv EpcAMxCD3 with M7 mutant in anti-CD3 part
 ; US-10-682-845-65

Query Match 47.7%; Score 701; DB 4; Length 492;
 Best Local Similarity 51.6%; Pred. No. 2.9e-41;
 Matches 148; Conservative 28; Mismatches 59; Indels 52; Gaps 7;

SEQ ID NO 79
 ; LENGTH: 492
 ; TYPE: PRT
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: scFv EpcAMxCD3 with M31 mutant in anti-CD3 part
 ; US-10-682-845-79

Query Match 47.7%; Score 701; DB 4; Length 492;
 Best Local Similarity 51.9%; Pred. No. 2.9e-41;
 Matches 149; Conservative 28; Mismatches 58; Indels 52; Gaps 8;

Qy 2 AQVQLQSGAELARPAGSVKMSCKASGTTFTTYHVRQPHDLEWIGYINPSSGYSD 61
 Db 243 SDILQQLQSGAELARPAGSVKMSCKASGTTFTTYHVRQPHDLEWIGYINPSSGYTN 302

Qy 62 YNQNFKGKTTLTADKSNTAYMOLNSLTSEDSAVYYCARRADYGNEYTWFAWGOCTTV 121
 Db 303 YNQKFKDATLTIDKSSTAYMOLNSLTSEDSAVYYCARRYE-GRY --CLOYWGQGTTL 358

Qy 122 TWSAAKTRPKLGG-----DQAVVTOESA-LITSPGETTLTCRSNTGTVT 166
 Db 359 TVSSVE----GGSGGGSGGGCVDDIQ--LTQSPAIMSASPGEKVTMTCRASSV-- 409

Qy 167 TSNTANWQEKPDHLFTGLIGHTNRAFGVPARFSGLIGDKAALITGAQTEDEAATYFC 226
 Db 410 --SYMANTWQQKSOTSPRKWIYDTSKVASSGVPRFGSGSGTTSYLTSSMEEADARTYFC 467

Qy 227 ALWNNNHVFGGGTKLAVLGQPKSAAAGSEOKLISEEDLNHHHHH 273
 Db 468 QQMSNPFLFGAGTKELED-----KHHHHHH 492

Search completed: February 9, 2006, 03:59:48
 Job time : 128.57 secs

RESULT 15
 US-10-682-845-79
 ; Sequence 79, Application US/10682845
 ; Publication No. US2004016241A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lanaveccchia, Antonio
 ; TITLE OF INVENTION: Potent T cell modulating molecules
 ; FILE REFERENCE: G2246 US
 ; CURRENT APPLICATION NUMBER: US/10/682,845
 ; CURRENT FILING DATE: 2003-10-10
 ; PRIOR APPLICATION NUMBER: US 60/419,149
 ; PRIOR FILING DATE: 2002-10-19
 ; PRIOR APPLICATION NUMBER: CA 2,403,313
 ; NUMBER OF SEQ ID NOS: 89
 ; SOFTWARE: PatentIn version 3.1

Result No.	Score	Query	Match	Length	DB ID	Description
1	683.5	/cgm2_6/prodata/2/pubpaas/US00_NEW_PUB_pep:**	249	7	US-11-054-515-1838	Sequence 1838, Ap
2	676.5	/cgm2_6/prodata/2/pubpaas/US00_NEW_PUB_pep:**	245	7	US-11-054-515-1823	Sequence 1523, Ap
3	674.0	/cgm2_6/prodata/2/pubpaas/US00_NEW_PUB_pep:**	615	6	US-10-012-184-50	Sequence 50, Appl
4	668.5	/cgm2_6/prodata/2/pubpaas/US05_NEW_PUB_pep:**	290	7	US-11-032-773-957	Sequence 957, App
5	660.5	/cgm2_6/prodata/2/pubpaas/US10_NEW_PUB_pep:**	44.9	7	US-11-054-515-1939	Sequence 1919, Ap
6	659.0	/cgm2_6/prodata/2/pubpaas/US10_NEW_PUB_pep:**	319	7	US-11-032-773-955	Sequence 955, App
7	654.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	250	7	US-11-054-515-1722	Sequence 1722, Ap
8	651.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	247	7	US-11-054-515-948	Sequence 948, Ap
9	651.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	248	7	US-11-054-515-1643	Sequence 1643, Ap
10	651.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	250	7	US-11-054-515-1723	Sequence 1723, Ap
11	650.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	247	7	US-11-054-515-927	Sequence 927, App
12	649.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	248	7	US-11-054-515-893	Sequence 893, App
13	647.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	44.0	7	US-11-054-515-1681	Sequence 1681, Ap
14	646.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	251	7	US-11-054-515-1496	Sequence 1496, Ap
15	646.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.9	7	US-11-054-515-2082	Sequence 2082, Ap
16	644.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.8	7	US-11-054-515-1688	Sequence 1688, Ap
17	644.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	248	7	US-11-054-515-1609	Sequence 1609, Ap
18	643.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.8	7	US-11-054-515-1459	Sequence 1459, Ap
19	643.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.7	7	US-11-054-515-1679	Sequence 1679, Ap
20	642.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.7	7	US-11-054-515-1936	Sequence 1936, Ap
21	640.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.6	7	US-11-054-515-1939	Sequence 1939, Ap
22	640.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	248	7	US-11-054-515-1622	Sequence 1622, Ap
23	639.5	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.5	7	US-11-054-515-1660	Sequence 1660, Ap
24	639.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.5	7	US-11-054-515-1670	Sequence 1670, Ap
25	639.0	/cgm2_6/prodata/2/pubpaas/US60_NEW_PUB_pep:**	43.5	7	US-11-054-515-1755	Sequence 1755, Ap

Db 61 AERLOGRVTIADELTRVNMELSSERDATTAVYCARESEGGDTNP - FGYWGRGTTVT 119 Qy 236 FGGTKLTVLG 246
 Db 123 VS---SAKTPKLGDDIONVTOESALTSRGETVTLTCSRNTGTYTTSNANWQEK 177 Db 235 FGGTKLTVLG 245
 Db 120 VSSGGSGGGGGGGSAQAQVVIQEPSLTVSPGTVTLCSTSAGTAVNNNTPSWFQOK 179
 Result 3 US-10-512-184-50
 Qy 178 PDHLFTGLIGHTNNNAPGVDFRSGLIGKAALITGAOTDEAYFCALWVN-HWVF 236 ; Sequence 50, Application US/10512184
 Db 180 PGQAPRPLISWTNNRPSWTPARFSAYLLGKAVTLGSQVPEDEAYCYCLYSGDAQLV 239 ; Publication No. US20050244901A1
 General Information:
 ; APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V
 ; TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease
 ; TITLE OF INVENTION: antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated Plant disease
 ; FILE REFERENCE: 1581-01US01
 ; CURRENT APPLICATION NUMBER: US/10/512,184
 ; CURRENT FILING DATE: 2004-10-22
 ; NUMBER OF SEQ ID NOS: 72
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 50
 ; LENGTH: 615
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: fusion protein
 ; CURRNT FILING DATE: 2004-06-18 ; OTHER INFORMATION: comprising the leader peptide - chitinase - linker
 ; APPLICANT: Ruben et al. ; OTHER INFORMATION: - cmyc/His6.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/233,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO: 1523
 ; LENGTH: 245
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-054-515-1523

RESULT 2 US-11-054-515-1523
 Sequence 1523, Application US/11/054515
 Publication No. US20050255532A1
 General Information:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; CURRENT APPLICATION NUMBER: US/11/054,515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543,296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580,347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/233,418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO: 1523
 ; LENGTH: 245
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-054-515-1523

Query Match 46.0%; Score 676.5; DB 7; Length 245;
 Best Local Similarity 56.6%; Pred. No. 7.3e-37;
 Matches 142; Conservative 27; Mismatches 69; Indels 13; Gaps 4;

Result 4 US-11-032-773-957
 Sequence 957, Application US/11/032773
 Publication No. US20060018911A1
 General Information:
 ; APPLICANT: Levy, Ronald
 ; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
 ; FILE REFERENCE: 17101-013001 / 1762
 ; CURRENT APPLICATION NUMBER: US/11/032,773
 ; CURRENT FILING DATE: 2005-01-11
 ; PRIOR APPLICATION NUMBER: 60/536,184
 ; PRIOR FILING DATE: 2004-01-12
 ; PRIOR APPLICATION NUMBER: 60/557,591
 ; PRIOR FILING DATE: 2004-03-29
 ; NUMBER OF SEQ ID NOS: 958
 ; SOFTWARE: FastSSO for Windows Version 4.0
 ; SEQ ID NO: 957
 ; LENGTH: 290

; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PBAD S1C5 V5 His protein sequence
 US-11-032-773-957
 Query Match 45.5%; Score 668.5; DB 7; Length 290;
 Best Local Similarity 50.0%; Pred. No. 2.7e-36;
 Matches 147; Conservative 38; Mismatches 84; Indels 25; Gaps 7;
 Qy 1 MAQVOLQSGAELARPAGAVRMSKRSAGTYETTYIHWVRQPHDLEWIGYINPSSGYS 60
 Db 1 MAEVQLQSGAELVPGAVSIVSKRSAGTYETDYHWRQPRBPELWIGPISPGNDI 60
 Qy 61 DYNQNPFGKTLTADKSSNTAYMQLNSLTSSEDAVYCARRADYGNYEYTWFAYNGQQTT 120
 Db 61 RYNEKEKDQKATLTADKSSNTAYMQLNSLTSSEDAVFCRSFYY--YDNQGDYNGQQTT 118
 Qy 121 VTVSSAKTT-----PKLGDIQAVVTQSSA-LTTSPEGTVLTCRNTGTVTISNYA 171
 Db 119 LTVSSSGAPGGGSGGGSDIVLTQSPAIMSALEERVMTCTASS--VSSSYF 176
 Qy 172 NWVQEKPDHLFTGLIGHTNNPAPGVPARFSGLIGDKAALTITGAOTEDEAYFCALWYN 231
 Db 177 HWYQQKPGPSSPKLWYTTSNIALSGVPARFSGSGTSYSLTSSMEAATYCHQYHR 236
 Qy 232 NHWVFGGGTKLTVL---GQPKSAAGS----EQKLISEEDLNS--EHHHHHH 273
 Db 237 SPLTFGAGTKLKLRAADAFTVSAASAFLGKPIPNPLGLDSTNSAVDHHHHH 290
 RESULT 5
 ; Sequence 1919, Application US/11054515
 ; Publication No. US2005055532A1.
 ; CURRENT APPLICATION NUMBER: US/11/054.515
 ; CURRENT FILING DATE: 2005-02-10
 ; PRIOR APPLICATION NUMBER: 60/543, 296
 ; PRIOR FILING DATE: 2004-02-11
 ; PRIOR APPLICATION NUMBER: 60/580, 347
 ; PRIOR FILING DATE: 2004-06-18
 ; PRIOR APPLICATION NUMBER: 10/293, 418
 ; PRIOR FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/331, 469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340, 817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880, 748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293, 499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277, 379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276, 248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240, 816
 ; PRIOR FILING DATE: 2000-10-17
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 3247
 ; LENGTH: 245
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-054-515-1919
 Query Match 44.9%; Score 660.5; DB 7; Length 245;
 Best Local Similarity 54.5%; Pred. No. 7.6e-36;
 Matches 138; Conservative 34; Mismatches 64; Indels 17; Gaps 5;

Qy 3 QVOLQSGAELARPAGAVRMSKRSAGTYETTYIHWVRQPHDLEWIGYINPSSGYS 62
 Db 1 EVQLVQSGAEVKPGAVSIVSKRSAGTYETDYHWRQPRBPELWIGPISPGNDI 60
 Qy 63 NONFRGKTLTADKSSNTAYMQLNSLTSSEDAVYCARRADYGNYEYTWFAYNGQQTT 124
 Db 61 AQKPQGRVTTMDTSTSTSYMELSLRSEDTAVYCARDLS-GSYFSRVDYNGQGTLYT 111
 Qy 123 VSS---AKTPPKLGDIQAVVTOESALTTPGETVTLCRSNTGTVTISNYAWQKEKD 177
 Db 120 VSSGGGGGGGGGGSELTDQPAVSVALGVNVRTCQ---GDSLRSYYASYTQQQKPG 177
 RESULT 6
 ; Sequence 955, Application US/11032773
 ; Publication No. US2006018911A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ault-Riche, Dana
 ; LEVY, Ronald
 ; TITLE OF INVENTION: DESIGN OF THERAPEUTICS AND THERAPEUTICS
 ; FILE REFERENCE: 17102-013001 / 17622
 ; CURRENT APPLICATION NUMBER: US/11/032,773
 ; CURRENT FILING DATE: 2005-01-11
 ; PRIOR APPLICATION NUMBER: 60/536,184
 ; PRIOR FILING DATE: 2004-01-12
 ; PRIOR APPLICATION NUMBER: 60/557,591
 ; PRIOR FILING DATE: 2004-03-29
 ; NUMBER OF SEQ ID NOS: 938
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 955
 ; LENGTH: 319
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PBAD S1C5 CD20 His Protein Sequence
 US-11-032-773-955
 Query Match 44.8%; Score 659; DB 7; Length 319;
 Best Local Similarity 45.8%; Pred. No. 1.2e-35;
 Matches 148; Conservative 38; Mismatches 83; Indels 54; Gaps 1
 Qy 1 MAQVOLQSGAELARPAGAVRMSKRSAGTYETTYIHWVRQPHDLEWIGYINPSSGYS 60
 Db 1 MAEVQLQSGAELVPGAVSIVSKRSAGTYETDYHWRQPRBPELWIGPISPGNDI 60
 Qy 61 DYNQNPFGKTLTADKSSNTAYMQLNSLTSSEDAVYCARRADYGNYEYTWFAYNGQQTT 12
 Db 61 RYNEKEKDQKATLTADKSSNTAYMQLNSLTSSEDAVFCRSFYY--YDNQGDYNGQQTT 11
 Qy 121 VTVSSAKTT-----PKLGDIQAVVTOESA-LTTSPEGTVLTCRNTGTVTISNYA 17
 Db 119 LTVSSSGAPGGGGGGGGGGDIVLTQSPAMSASLBERTVMTCTASS--VSSSYF 17
 Qy 172 NWVQEKPDHLFTGLIGHTNNPAPGVPARFSGLIGDKAALTITGAOTEDEAYFCALWYN 23
 Db 177 HWYQQKPGPSSPKLWYTTSNLASGPARGSGSGTSYSLTISMAEADATYCHQYHR 23
 Qy 232 NHWVFGGTKLTVL---GOPKSAAGSOKL---I-SEEDLN----- 26
 Db 237 SPLTFGAGTKLEKRAADAFTVSAASFLKISHMELNFIRAFTPYININYCEPANP 29
 Qy 267 -----SHHHHHH 273
 Db 297 SEKISPSTOCYNSAVDHHHHHH 319

RESULT 7
US-11-054-515-1722
Sequence 1722, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/240,816
Remaining Prior Application data removed - See File Wrapper or PALM.
SEQ ID NO: 3247
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO: 1722
LENGTH: 250
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-1722
Remaining Prior Application data removed - See File Wrapper or PALM.

Query Match 44.5%; Score 654; DB 7; Length 250;
Best Local Similarity 53.3%; Pred. No. 2e-35;
Matches 137; Conservative 35; Mismatches 65; Indels 20; Gaps 5;

Query Match 44.3%; Score 651.5; DB 7; Length 247;
Best Local Similarity 54.3%; Pred. No. 2.8e-35;
Matches 138; Conservative 34; Mismatches 65; Indels 17; Gaps 5;

Qy 3 QVQLQSGAEELARPAGASVYKMSCKASGVTETTYTILHYWRQPGHDLENVIGYINPSGSYD
Db 1 QVQLQSGAEEVKPGASVYKMSCKASGVTETSYCISWRQAPGQGLERNGWMNPNSGNTGY 60
Qy 63 NQNPKGKTTLTADKSNTAYMQNLSLTSEDSAYYCARRADY---EYTWPAYNGQ 117
Db 61 AQRFQGRVTTMTNTSTAYMELSLRSRDTAVYFCAR---GQYQDILTGDNWDPGK 116
Qy 118 GRTTVYSS---AKTPKGKGGDIOAVYTOESALITSPGETVTLTCRSNTGTVTNSYAWV 174
Db 117 GTLVSVGGGGGGGGGGSSSELTDPAVSALGVTRITCQ---GDSLRSYYASWY 173
Qy 175 QKEPDHLPTGLIGHTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEALYFCAL--WYNN 232
Db 174 QQKEGOAPVLVITYGKNNRPSGVDRFGSSSGNTASLTITGAODEADYYCNXRDSGGN 233
Qy 233 HWYFGGTTKLTVLG 246
Db 234 HYVFGGTTKLTVLG 247
RESULT 9
US-11-054-515-1643
Sequence 1643, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18

RESULT 8
US-11-054-515-948
Sequence 948, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3

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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or P.A.M.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 1723
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1723

Query Match          44.3%; Score 651; DB 7; Length 250;
Best Local Similarity 52.9%; Pred. No. 3.1e-35;
Matches 136; Conservative 36; Mismatches 65; Indels 20; Gaps 5;
Query 3 QVQLQSGAELARPGAVKNSCKASGTYFITYIHWQRQPHDLEWIGYINSSGYSID 62
Db      1 EVQLQSGAEVREPGAVKVSCKASGTYFTGYMHWRQAPGQLEWGNWINSGGTNY 60
Query 63 NQNPKGKTUTADKSSNTAYMOLNLSLTSDESAVYCARRADY ---GNYEYTWFAYMGOG 118
Db      61 AQKFCQGRVMTRDTSISTAYMELSRRLRSDDTAVYCARVLPHYDILITYSQSNWFPWGKG 120
Query 119 TTVTVS---ARTTPKLGGDIAQAVVTTQESALTTSPGETVTLTCRSTNTGTVTTSMYANWQ 175
Db      121 TMVTTISGGGGGGGGSSSELTODPAYSVALLGQTVRITCQ--GDSSLRSYSTASYQ 177
Query 176 EKPDHILFTGLIGHTNRNAPGTYPARFGCSLIGDKAALITGQAQTEDAYFCALMWN--- 231
Db      178 QKPGQAPVLVYTKRNRSQGIPDRFSGSSSGNTASLTITGAQREDAKYC---NSRDS 233
Query 232 -NHWTFGGTQLTVLG 246
Db      234 SGNRYVFGGGTQLTVLG 250

RESULT 11
US-11-054-515-927
; Sequence 927, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
;   APPLICANT: Ruben et al.
;   TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLYs
;   CURRENT APPLICATION NUMBER: US/11/054-515
;   CURRENT FILING DATE: 2005-02-10
;   PRIOR APPLICATION NUMBER: 60/543,296
;   PRIOR FILING DATE: 2004-02-11
;   PRIOR APPLICATION NUMBER: 60/580,347
;   PRIOR FILING DATE: 2004-06-18
;   PRIOR APPLICATION NUMBER: 10/293,418
;   PRIOR FILING DATE: 2002-11-14
;   PRIOR APPLICATION NUMBER: 60/331,469
;   PRIOR FILING DATE: 2001-11-16
;   PRIOR APPLICATION NUMBER: 60/340,817
;   PRIOR FILING DATE: 2001-12-19
;   PRIOR APPLICATION NUMBER: 09/880,748
;   PRIOR FILING DATE: 2001-06-15
;   PRIOR APPLICATION NUMBER: 60/293,499
;   PRIOR FILING DATE: 2001-05-25
;   PRIOR APPLICATION NUMBER: 60/277,379
;   PRIOR FILING DATE: 2001-03-21
;   PRIOR APPLICATION NUMBER: 60/276,248
;   PRIOR FILING DATE: 2001-03-16
;   PRIOR APPLICATION NUMBER: 60/240,816
; Remaining Prior Application data removed - See File Wrapper or P.A.M.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO: 927
; LENGTH: 247

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1 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-927

Query Match 44.3%; Score 650.5; DB 7; Length 247;
 Best Local Similarity 53.9%; Pred. No. 3 3e-35;
 Matches 137; Conservative 35; Mismatches 65; Indels 17; Gaps 5;

Qy 3 OVOLOQSGAELARPGAVSKVSKASGYTFTTYIHWYRQRPCHDLEWIGYNINPSSGYSDY 62
 Db 1 OVOLOQSGAEVKPGAVSKVSKASGYTFTSYGSIWYRQAPCGLEWMGNNPNSNTGY 60

Qy 63 NONFRGKTTLADKSSNTAYMOLNSLTSEDASVYCAR-----RADYGNYEYTWFAYWG 116
 Db 61 AQKFQGRVTITADESTSTAYMELSLRSEDTAVYCARMYDILTCYGGY---FDYWG 116

Qy 117 QGTTVYSS --AKTPKLGDDIQAVVTOESALTSPEGETYLITCRSNTGTVTTSYANW 173
 Db 117 QGTLTVSSGGGSGGGSSELTDOPAVSVALGTIVTCQ---GDSLRSYYASW 173

Db 174 VQEKPDLHFLTGDTIGHTNNRAFPVAFSGSLIGDKAALTITGAOTEDEAYFCALWYN-- 231
 Qy 174 YQQKQAPVLYIYGKRNPSGPDRFGSSSGNATSLITGAQAEDEADYTC---NSR 229

Qy 232 ---NHWVFGGGTKLTVLG 246
 Db 230 DSSGNVVEGGTKLTVLG 248

RESULT 13-054-515-1681
 Sequence 168;, Application US/11054515
 Publication No. US2005025532A1
 GENERAL INFORMATION:
 APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 FILE REFERENCE: PP523P3
 CURRENT APPLICATION NUMBER: US/11/054,515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543,296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580,347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293,418
 PRIOR FILING DATE: 2002-11-14
 PRIOR APPLICATION NUMBER: 60/331,469
 PRIOR FILING DATE: 2001-11-16
 PRIOR APPLICATION NUMBER: 60/340,817
 PRIOR FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 09/880,748
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 3247
 SEQ ID NO 893
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-054-515-893

Query Match 44.0%; Score 647; DB 7; Length 248;
 Best Local Similarity 53.5%; Pred. No. 5.5e-35;
 Matches 137; Conservative 36; Mismatches 63; Indels 20; Gaps 6

Qy 3 OVOLOQSGAELARPGAVSKVSKASGYTFTTYIHWYRQRPCHDLEWIGYNINPSSGYSDY 62
 Db 1 OVOLOQSGAEVKPGAVSKVSKASGYTFTSYGSIWYRQAPCGLEWMGNNGSPTRK 60

Qy 63 NONFRGKTTLADKSSNTAYMOLNSLTSEDASVYCARRADYG---NEYTYWFAYWGQT 119
 Db 61 SRKFQGRVTITKDSSAAAMELSSUGSEDTALYCA-RATYDPGLTGSYPSDFDINGRT 119

Qy 120 TVTVSS --AKTPKLGDDIQAVVTOESALTSPEGETYLITCRSNTGTVTTSYANWQE 176
 Db 120 LTVVSSGGGSGGGSSELTDOPAVSVALGTIVTCQ---GDSLRSYYAQWQQ 176

Qy 177 KPDHLFTGLIGHTNNRAPGVPARFGSLLIGDKALTIGAQTDEAIYFCALMWN---- 231
 Db 177 KPGAPVPLVYGNRPSCPIDPDRSGSSGNTSLITVQAADDAYC---NSRUSS 232
 Qy 232 -NHWVFGGTKLTVLG 246
 Db 233 GHNVVFGGTKLTVLG 248

RESULT 14

US-11-054-515-1496
 ; Sequence 1496, Application US/11054515
 ; Publication No. US2005025532A1

GENERAL INFORMATION:

APPLICANT: Ruben et al.
 TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

CURRENT APPLICATION NUMBER: US/11/054, 515
 CURRENT FILING DATE: 2005-02-10
 PRIOR APPLICATION NUMBER: 60/543, 296
 PRIOR FILING DATE: 2004-02-11
 PRIOR APPLICATION NUMBER: 60/580, 347
 PRIOR FILING DATE: 2004-06-18
 PRIOR APPLICATION NUMBER: 10/293, 418
 PRIOR FILING DATE: 2004-11-14
 PRIOR APPLICATION NUMBER: 60/331, 469
 PRIOR FILING DATE: 2004-11-16
 PRIOR APPLICATION NUMBER: 60/340, 817
 PRIOR FILING DATE: 2004-05-19
 PRIOR APPLICATION NUMBER: 10/293, 418
 PRIOR FILING DATE: 2004-11-14
 PRIOR APPLICATION NUMBER: 60/331, 469
 PRIOR FILING DATE: 2004-11-16
 PRIOR APPLICATION NUMBER: 60/340, 817
 PRIOR FILING DATE: 2004-12-19
 PRIOR APPLICATION NUMBER: 09/880, 748
 PRIOR FILING DATE: 2001-06-15
 PRIOR APPLICATION NUMBER: 60/293, 499
 PRIOR FILING DATE: 2001-05-25
 PRIOR APPLICATION NUMBER: 60/277, 379
 PRIOR FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/276, 248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/240, 816
 PRIOR FILING DATE: 2001-10-17
 Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 3247

SEQ ID NO: 2082

TYPE: PRT
 ORGANISM: Homo sapiens

Query Match 43.9%; Score 646; DB 7; Length 254;
 Best Local Similarity 51.6%; Pred. No. 6.5e-35;
 Matches 131; Conservative 35; Mismatches 78; Indels 10; Gaps 3;

Qy 3 QVQLOQSGAELRPAVSNSCKASGYTFTTYHWRQRPGHLEWIGYINPSSGGSDY 62
 Db 1 QVQLVQSGADVKKPCASVRSKASGYTFTSHYHWRQAPGRGLEWMGVINPSGATNY 60

Qy 63 NQNFPGKTTLTDKSSNTAYMQLNSLSEDAVYCARRADYGNB---YTWFATWGQGT 119
 Db 61 AQKFQGRVTMTRDSTSSTVMELOSSLRFEPETAYTCVRDAEGLVEAETNWFDWGQGT 120

Db 120 TVTVS---SAKTPKLGGDIQAVYTQESALTSPGETVTLTCRSNTGTVTTSNYANWV 174
 Qy 121 MVTUSSGGSSGGGGSAQSVLTQEPSVSGAPGQRTISCTGGSSNIGASYDVNWY 180
 Db 122 QEKPHLFLCLIGHTNNRAPGVPARFGSLLIGDKALTIGAQTDEAIYFCALMWN-N 232
 Qy 123 NQNFPGKTTLTDKSSNTAYMQLNSLSEDAVYCARRADYGNB-YTWF-AWGGQGT 120
 Db 124 SQKLQGRTVTRDISASTAMELSSURSEDAVYCA-RSDYDLTGYTWWPATWGQTM 119
 Qy 125 VTVS----SAKTPKLGGDIQAVYTQESALTSPGETVTLTCRSNTGTVTTSNYANWQ 175
 Db 126 VTVSSGGGGGGGGGGGGSAQSVLTQOPPSASGSPEQSVTISCTGGSYVSWYQ 179
 Qy 127 BKPDLHFTGLIGHTNNRAPGVPARFGSLLIGDKALTIGAQTDEAIYFCALWY-NTHW 234
 Db 128 QPGKAKPLIVNEVRPSGVPDRSGSKSENTASLTVSGLQADEAINTYCASTVGNWV 239

Db 129 VEGGTGXLTIVLG 246
 Db 130 VFGGTGXLTIVLG 254

Search completed: February 9, 2006, 04:00:32
 Job time : 20.909 sec

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